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SITSVLAWTAILATLEFVYRKPONEDQKYKCAFSRTPELFADETFWKHFLTLKWNI
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EHFSLEDCKSSYNLOKSVHTTKLIATTHCCINPLLYAFLDGTFSKYLCRCFHLRSNTF
LQPRGQSAQGTSREEDDHSTEV"
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      Gish,K., McClanahan,T.K. and Moore,K.W.
CRAM: A Novel Human Chemokine Receptor-Like Gene Expressed in
Activated Monocytes
Unpublished
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/cell_type="primary monocytes; activated"
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                                                                                                                        2 (bases 1 to 1546)
Gish,K., McClanahan,T.K. and Moore,K.W.
Direct Submission
Submitted (22-JUL-1997) Molecular Biology, D
901 California Avenue, Palo Alto, CA 94304,
Location/Qualifiers
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/db_xref="GI:3550067"
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/db_xref="taxon:9606"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 1146)
GCAGTITCTAACTIGTGTTTCTTGCTDACCCTGCCCTTCTGGGCTCATGCTGGGGGCGAT
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
868 TGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTCTGGAAGCATTTTCTG
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                                                                                                                                                                                                                           1048 TTTGCCGTAATGGTAGTCTTCCTTCTGATGTGGGCCCCCTACAATATTGCATTTTTCCTG
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Sequence 15 from Patent WO0208284.
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CSAVEVIGULDNLLVVLILYKKGLKRYENYILILALSVSICETLITEPPRAHAGGDPM
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REBPDHSTEV"
                                                                                                                             Gish,K., McClanchan,T.K. and Moore,K.W.
Direct Submission
Submitted (22-U10)
901 California Avenue, Palo Alto, CA 94304, USA
Location/Qualifiers
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 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1790)
Gish, K., McClanahan, T.K. and Moore, K.W.
CRAM: A Novel Human Chemokine Receptor-Like Gene Expressed
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11arity 100.0%; Pred. No. 2.8e-284;
Conservative 0; Mismatches 0; Indels 0:
                                                                                                                                                                                                                                                                                                                       /map="3p21.3"
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1. .1790
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328. .1362
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                                                                              Activated Monocytes
                                                                                          Unpublished
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Matches 1035; Conserv
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0200690-0.A 15 03-JAN-2002;
Genenech, Inc. (US)
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Pred. No. 2.3e-283;
0; Mismatches 2;
                                                                                              DNA

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                                                                                        Sequence 15 from Patent WO0200690. AX490908
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1049 TCCACCGAAGTGTAA 1063
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Best Local Similarity 99.8%;
Matches 1033; Conservative (
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Homo sapiens
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Query Match 99.7%; Score 1031.8; DB 6; Length Best Local Similarity 99.8%; Pred. No. 2.3e-283; Matches 1033; Conservative 0; Mismatches 2; Indels
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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larity 99.8%; Pred. No. 2.3e-283;
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/db_xref="taxon:9606"
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Location/Qualifiers
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|TCCACCGAAGTGTAA 1063
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Mammalia; Butheria; Primates; Catarrhini; Homínidae; Homo.
                                                                                      TTTGCCATAATGGTAGTCTTCCTTCTGATGTGGGCGCCCCTACAATATTGCATTTTTCCTG
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Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such
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iive 0; Mismatches 2;
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Patent: WO 02061087-A 353 08-AUG-2002;
Lifespan Blosciences, Inc. (US)
Location/Qualifiers
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Seguence 353 from Patent WO02061087.
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/mol type="unassigned DNA"
/db xref="taxon:9606"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 2.3e-283;
0; Mismatches 2; Indels
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Receptor proteins
Patent: WO 2004083232-A 1 30-SEP-2004;
Oxagen Limited (GB)
                                                                                         Location/Qualifiers
1. .1645
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 99.8%;
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Latlpeyvykpqmedqkykcafscppplplakgnpfplilkmisulvlpleiffp
Lyqqrkylbregysyslkkupfainvyfllamapymiapflsffrenesledksy
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                                    2 [bases 1 to 1698]
Ansari-Lari, M.A., Liu, X.-M., Gorrell, J.H. and Gibbs, R.A.
Direct Submission
Submitted (18-JUL-1997) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Location/Qualifiers
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Pred. No. 2.3e-283;
0; Mismatches 2;
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protein_id="AAB82106.1"
db_xref="G1:2305264"
nember of chemokine receptor gene family
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                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
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/chromosome="3"
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/note="either
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/gene="CKRX"
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1677. .1682
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/gene="CKRX"
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Best Local Similarity 99.8%;
Matches 1033; Conservative
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/cell_type=
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  Eukaryogia, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases I to 1698)
Ansari-Lari,M.A., Liu,X.-M., Gorrell,J.H. and Gibbs,R.A.
Haplotype analysis of a gene cluster containing CCR5 and a new
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                                                              GCAGTTTCTAACTTGTGTTTCTTGCTTACCCTGCCCTTCTGGGCTCATGCTGGGGGGGAT
                                                                                                                                                    CCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTACAGTGAGACATTTTTC
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                                           GCAGTTTCTAACTTGTGTTTTCTTGCTTACCCTGCCCTTCTGGGGCTCATGCTGGGGGGGAT
                                                                                                                          CCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTACAGTGAGACATTTTTC
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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.E., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N. K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Haieh, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M. B., Bondido, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Youchman, J.W., Green, E.D.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Saniutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Land, M. Schein, J. B., Jones, S.J. and Marra, M.A.
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Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupca,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McCloskell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,J.W.
                                                        ACCCCACTTCAACCCAGGGGGGGGTCTGCACAAGGCACATCGAGGGAAGAACCTGACCAT 1020
                                                                                                                                                                                                                                                                                                                    2, mRNA (cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1770)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Ensil: cgapbs-r@mail.nih.gov
EDNA Library Preparation: Life Technologies, Inc.
EDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
                                                                                                                                                                                                                                                                                                 Homo sapiens chemokine (C-C motif) receptor-like clone MGC:34104 IMAGE:5228561), complete cds.
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Homo sapiens
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LLYQMKTTLRFREGRYSLFKLVPAIMVVFLLMMAPYNIAFFLGTFKEHFSLSDCKSSY
NLYKSVHITKLIATTHCCINPLLYAFLDGTFSKYLCRCFHLRSNTPLQPRGGSAQGTS
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Pred. No. 2.3e-283;
0; Mismatches 2; Indels
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Best Local Similarity 99.8%;
Matches 1033; Conservative
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Young, P.B., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature gene sets Patent: WO 0194629-A 6461 13-DEC-2001; Avalon Pharmaceuticals (US)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                      734 TGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTCTGGAAGCATTTTCTG
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Pred. No. 2.8e-283;
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AX335952
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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SAVEYIGYULDNLLVVLILYKKGLKRYENIYLLALAVSULCELLIEPWAHAGODPM
CKILIGLYPYGLYSETEPWCLLTYQRYLVFLHKGNFFSARRYPCGIITSVHAVTA
LATLPEYVYKRQMEDOKYKCAFSRTPFLFBADETFWKHFLTLKWNISVLYLPLFIFT
LLYQWRKTLARREQRYSLPKLVPAIWYVFLLMWAPYNIAFFLSTFKEHFSLSCKSSY
RLDKSVHITKLIATTHCCINPLLYAFLDGTFSKYLCRCFHLRSNTPLQPRGQSAQGTS
REBPDHSTEW"
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 49 Row: o Column: 13
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 14043058.
Location/Qualifiers
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                                                                                                                                                                                            /tissue type="Pancreas, Spleen, adult pooled"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   motif) receptor-like
                                                                                                                                                                                                                                                                      1. .1770
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                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                      194. .1228
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99.8%;
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Best Local Similarity 99.8
Matches 1033; Conservative
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/gene="ccr2"
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/note="confirmed by similarity to Human monocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="ccr2a"
//product="ccr2a"
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chemoattractant protein 1 receptor (ccr2) alternatively
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="confirmed by similarity to Human monocyte chemostractant protein 1 receptor (ccr2) alternatively spliced A-form, Encoded by GenBank Accession Number U80924, gi 1168965"
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spliced mRNA encoding B-form carboxyl tail. Accession
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Regions with single-strand coverage are as follows:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31434 - 31443 37900 - 37968 53303 - 53357 59166 - 59206 63708 - 63988 65200 - 65335 78655 - 78713 92135 - 92137 112377 - 112551 112643 - 1127784 - 134069 - 134068 - 144068.
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1. .143068
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                                                                             Homo sapiens (human)
                                                                                              Homo sapiens
                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                 GCAGTTTCTAACTTGTGTTTTCTTGCTTACCCTGCCCTTCTGGGCTCATGCTGGGGGCGAT
                                                                                                                                                                                                                                                         96942 CCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTACAGTGAGACATTTTTC
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         GAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCCCAGGCACTCTCAGCCCAGCTG
                                                                 GTGCCATCACTCTGCTGTGTGTTTGTGATCGGTGTCCTGGACAATCTCCTGGTTGTG
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HSU95626 143068 bp DNA linear PRI 16-MAY-1997 Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6

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Pred. No. 2.8e-283;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/product="lactoferrin"
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/evidence=not experimental
96642. .97676
/gene="ccr6"
96642. .97676
/gene="ccr6"
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SVITWLVAVFASVPGIIFTKQKEDSYVYGPFPRGNNNFHTIMRILIGLYLPLLIN
SVITWLVATTARAFTHARAFTHYTTILLILGLYLPLLIN
CESTSGILKTLLRCRNEKKRHRAVPITTIMITYPFFPVIVVILLNTFQEFFGLSN
CESTSGILGATGVTFTGGILDGRGKGSIGRAFFFFIFFITALGCRIAPLQFFFGCSP
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LPGII FTRGOKBGLHYTCSSHFPYSQYQFWRNFQTLKIVILGLVLPLLVMVICYSGIL
KTLIRCRNEKKRHRAVRLIFTIMIVYFLFWAPYNIVLLLNTFQEFFGLNNCSSSNRLD
QAMQYTETLGMTHCINPIIYAFVGEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPER
ASSVYTRSTGEQEISVGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVITMLVAVPASVPGIIFTKCCKEDSYYVCGPYFPRGANNFHTIMRNILGLVLPLIM
VICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWTPYNIVILLNTFQBFFGLSN
CESTSQLDQATQVTETLGMTHCCINPIIYAFVGEKFRRYLSVFFRKHITKRFCKQCPV
FYRETVDGVTSTNTFSTGEQEVSAGL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trānglation="MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFG
PVGNMLVILILINCKRLKSMTDIYLLNLAISDLPPLLTVPFWAHYAAAQWDFGNTMCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Identified as a gene by Grail Version 1.3c.
Translated sequence exhibits 42% sequence identity to CCR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /t-fanslation="manyTlapedeydvliegelesdeargcdkydagalsaglupesl
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cktliglyfyglyseffyclltygrylyflyfygresarrycycgiitsylmytal
latlebyyykpQmbockykcarsrpplearhethrythrolisyllyfyfffff
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NLDKSVHITKLIATTHCCINPLLYAFLDGTFSKYLCRCFHLRSNTPLQPRGQSAQGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANEWVPGNAMCKLFTGLYHIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVT
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/translation="MLSTSRSRPIRNTNESGEEVTTFFDYDYGAPCHKFDVKQIGAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="confirmed by similarity to human CC chemokine receptor 5 (ccr5) protein, encoded by GenBank Accession Number U54994, gi 1457946"
                                                                                                                                                                                                                                                   /ince="confirmed by similarity to Human monocyte chemoattractant protein 1 receptor (ccr2), Accession Number: 1168965"
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number: U54994."
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/gene="lactoferrin"
complement(join(124605. .124816,126528. .126717,
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/gene="ccr5"
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/evidence=not_experimental
/product="ccr6"
                                                                                                                                                                                                                                                                                                                                                   product="ccr2b"
|protein_id="AAB57792.1"
|db_xref="G1:2104519"
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/db_xref="GI:2104521"
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/db_xref="G1:2104520"
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This sequence Validation:

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinteing. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                              Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
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3': RP11-509121 (UWGC:bc0454) AC104304, 61294-bp overlap
Chemistry: Dye-terminator ET; 93% of reads Chemistry: Dye-terminator Big Dye; 7% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 184860 bases at least Q40 Consensus quality: 18538 bases at least Q30 Consensus quality: 18538 bases at least Q20 Insert size: 185437; sum-of-contigs Quality coverage: 7.6x in Q20 bases; sum-of-contigs
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Search completed: June 18, 2005, 09:52:53 Job time : 4763.26 Becs

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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AF405536 Macaca mu
AF291668 Macaca fa
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Cloning and expression of a new mcp receptor in glial cells
Patent: WO 02057779-A 32 25-UUL-2002;
Rijksuniversiteit Groningen (NL)
L. cation/Qualifiers
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//organism="Mus sp."
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Best Local Similarity 100.0%; Pred. No. 5.4e-260;
Matches 1083; Conservative 0; Mismatches 0; Indels 0;

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/note="mCCR12 chemokine receptor sequence"

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(c) 1993 - 2005 Compugen Ltd.
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1.0	SM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E 1 (bases 1 to 1793) S Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shemen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haleh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Sunin, G.M., Hong, L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Morker, K.J., Malek, J.A., Garcia, P.H., Richards, S., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Bontfara, A., Milting, M., Madan, A., Young, A.C., Shevchenko, Y., Rontfara, G., Milting, M., Madan, A., Young, A.C., Shevchenko, Y., Rontfara, G., Milting, M., Madan, A., Young, R.D., Rontfara, G., Milting, M., Madan, A., Young, Shevchenko, Y., Rontfara, G., Milting, M., Madan, A., Young, Shevchenko, Y., Rontfara, G., Milting, M., Madan, A., Young, Shevchenko, Y., Rontfara, G., Milting, M., Madan, A., Young, Shevchenko, Y., Rontfara, G., Milting, M., Madan, A., Young, Shevchenko, Y., Rontfara, G., Milting, M., Mang, M., M., Mang, M., M., Mang, M., M., M., M., M., M., M., M., M., M.	Dickson, M.C., Rodriguez, M.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Gorbert, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 2238827 12477932 2 (bases 1 to 1793) Straubberg, R. Direct Submission Submitted (15-OCT-2002) National Institutes of Health, Mammalian Submitted (15-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Marcello Bento Soares, Ph.D. Tissue Procurement: Marcello Bento Soares, Ph.D. CDNA Library Preparation: M. Bento Soares, University of Iowa CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemabiology.org contact: amadan@systemabiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Lubl at: http://image.llnl.gov Series: IRAK Plate: 83 Row: b Column: 2		/gene="Ccrl2" /gote="Stronymms: L-CCR, E01, CCRl1" /db_xref="LocusID:54199" /db_xref="LocusID:54199" /db_xref="MGI:1920904" 1781260 /gone="Ccrl2" /codon_start=1 /codon_start=1 /product="Ccrl2 protein" /protein_id="AAH38631.1" /db_xref="GI:24047249"
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A novel lipopolysaccharide inducible C-C chemokine receptor related
gene in murine macrophages
FEBS Lett. 425 (3), 490-494 (1998)
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Submission
Submitted (02-DBC-1997) Shizuo Akira, Hyogo College of Medicine,
Department of Biochemistry; Mukogawa-cho 1-1, Nishinomiya, Hyogo
663-8501, Japan (E-mail:akira@hyo-med.ac.jp, Tel:+81-798-45-6357,
Fax:+81-798-46-3164)
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Luo,Y., Berman,M.A., Fischer,F.R., Abromson-Leeman,S.R., Kuziel,W.A., Gerard,C. and Dorf,M.E.
RANTES and eotaxin stimulate chemotaxis, chemokine/cytokine synthesis, and receptor modulation in murine astroctyes
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/tissue type="TNF alpha treated bone marrow derived
dendritIc cells"
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Pred. No. 1.4e-259;
0; Mismatches 1;
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/mol_type="mRNA"
/strain="B10.BR"
                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
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Berman, M.A. and Dorf, M.E.
Direct Submission
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Best Local Similarity 99.9%;
Matches 1082; Conservative
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                                   Gaps
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; Score 1083; DB 10;
; Pred. No. 5.4e-260;
0; Mismatches 0;
 100.0%;
               Best Local Similarity 100.
Matches 1083; Conservative
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AC118727 169165 bp 'DNA linear ROD 24-JUL-2004 Mus musculus chromosome 9, clone RP24-166N8, complete sequence. AC118727 GI:50582829

DEFINITION ACCESSION VERSION

RESULT 5 AC118727 LOCUS

Direct Submassion

Direct Submassion

Direct Submassion

Submitted (10-ARR-2022) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Esses 1 to 169165)

Biren, B., Nusbaum, C., Lander, E., Abouellell, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Bogulaavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cooke, P., Corum, B., Collymore, J., Gode, S., Dooley, K., Dorris, L., Erickson, J., Rarco, S., Ferrelra, P., FilzGerald, M., Gage, D., Galagan, J., Hagoshan, B., Hall, J., Horton, L., Hulme, W., Illev, I., Hagoshan, D., Hagos, B., Hall, J., Horton, L., Mulme, W., Illev, I., Ganders, T., Callymon, R., Lindblad-Toh, K., Liud, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, U., Matchews, C., Macdonald, P., Major, J., Manning, U., Matchews, C., Connor, T., O'Donnell, P., Major, J., Raymasamy, U., Raymond, C., Phunkhang, P., Plerre, N., Rachupka, A., Ramasamy, U., Raymond, C., Connor, T., O'Donnell, P., O'Neal, D., Oliver, J., Peterson, K., Seaman, S., Severy, P., Smith, C., Spanner, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassalilev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zambek, L., Zimmer, A. and Zody, M., Zander, Cambridge, MA 02141, USA

Estera, Research, 320 Charles Street, Cambridge, MA 02141, USA

Estera, R., Sale, C., Cambridge, MA 02141, USA Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguelavkiy, L., Boukhalter, B., Camarata, J., Chang, J., Choopel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Brickon, J., Farco, S., Ferreira, P., Flzgerald, M., Gage, D., Gardyna, S., Graham, L., Grand-Plerre, N., Hafez, N., Hagoplan, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Mathews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., φ

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Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasany, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Steaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Toyohan, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Zimmer, A. and Zody, M.
                                                                                                                                                  Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@broad.mit.edu
Center project name: Listu4
Center clone name: Listu4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_"RP24-166N8"
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complement (310, .513)
/rpt_family="B4"
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/db_xref="taxon:10090"
/chromosome="9"
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Unpublished E (bases 1 to 230772) S Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazco, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArallano, K., Dewar, K., Diaz, J.S., Dodge, S., Farceira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illav, I., Johnson, R., Johnson, R., Jones, C., Kamet, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Jones, C., Kamet, A., Karatas, A., Kalls, C., Macdonald, P., Major, J., Matthews, C., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schugher, S., Schughes, R., Schugher, R., Schugher, R., Schugher, N., Schugher, N., Schauer, S., Schugher, N., Schauer, B., Stanger Thomann, N., Stojanovic, N., Talamas, J., Saringer, M., Schauer, S., Saringer, Thomann, N., Stojanovic, N., Talamas, J., Saringer, M., Schauer, S., Saringer, Thomann, N., Stojanovic, N., Talamas, J., Saringer, M., Schauer, S., Saringer, M., Schauer, S., Saringer, Thomann, N., Stojanovic, N., Talamas, J., Saringer, M., Saringer, S., Saringer, S., Saringer, J., Saringer, J., Saringer, M., Saringer, M., Saringer, S., Saringer, M., Saringer, M., Saringer, M., Saringer, S., Saringer, M., S	Viel.R., Vo.A., Wilson, B., Wu.X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Zembek, L., Zimmer, A. and Zody, M., Zembek, L., Zimmer, A. and Zody, M., Direct Submitted (14-58P-2012) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA. 3 (Dases I to 230772) Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choppel, Y., Collymore, A., Cooke, P., Corlum, B., Dedrellan, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Brickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N	nagopan, N., hadobis, hail, n., hollow, inline, i., i., hadopis, J., h	Vo.A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Zimmer, A. and Zody, M. Direct Submission Submitted (29-MAY-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 230772) Birren, B., Nubbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguelavkly, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeARellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Razo, S., Graham, L., Grand-Plerre, N., Hafez, N., Hagoplan, D., Hagoplan, D., Hagoplan, D., Hagoplan, D., Hagoplan, D., Hagoplan, D., Hagoplan, M., Ille, W., Ille, T., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Johnson, R., Jones, C., Kamate, A., Karates, A., Kells, C., Landers, T.,	Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Minova, T., Mlenga, V., Murphy, T., Naylor, J., Meneus, L., Minova, T., Micol, R., Norbu, C., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, R., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Stengan, S., Severy, P., Saman, S., Severy, P., Saman, S., Severy, D., Satho, C., Sporoce, B., Theodore, J., Stopan, K., Travers, M., Yasalise, H., Venkataraman, V.S., Viel, R., Voha, Wilson, B., Wu, X., Waman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission L. Submitted (22-JUL-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS		TITLE JOURNAL REFERENCE AUTHORS	TITLE
1980	541 CAGAAACACAGTGTGCCTTTGGCAAACCTCTTTGCCAATGGAGGGCCGCTCTGG 600 43105 CAGAAACACAAGTGTGCCTTTGGCAAACCTCACTTCTTGCCAATGGAGGCCGCTCTGG 43164 601 AAGTACGTTCTGACGTCAAAAATGATCATCTTGGTACTTTCCTCTGCTGCTTTTT 660 43165 AAGTACGTTCTGACGTCAAAAATGATCATCTTGGTACTTTCCTCTGCTGCTTTTTT 43224 661 ATAATCTGCTGCAGAGAAAATGATCATCTTGGTACTTTACCTCTCTGCTGCTTTTTT 4324 661 ATAATCTGCTGCAGAGAAAAATGATCATCTTGTACTTTACGGAGAAAAAGAGAAAAAAAA	43285 CHEMINICATION CHEM	43465	AC132832 230772 bp DNA linear ROD 23-JUL-2004 TION Mus musculus chromosome 9, clone RP23-48D19, complete sequence. NAC132832.13 GI:50540835 DS HTG. Mus musculus (house mouse) NISM Mus musculus (house mouse)

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/clone="RP23-48D19"
/clone_lib="RPCI-23 Female Mouse BAC"
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complement(1319. .1477)
/rpt_family="L2"
1909. .1966
                                                                                                                                                                                                                               1. .230772
/organism="Mus musculus"
                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="9"
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'rpt_family="ID_B1"
924, .404^
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complement (6959. .7065)
/rpt family="PB1D7"
complement (7667. .7817)
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omplement(5240. .5471)
rpt_family="B3"
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|318. .6670
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rpt_family="MIR"
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rpt_family="PB1"
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complement (751. .858)
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164._.1177
                                                                                                                                                                                                                                                                                                                                                                             /note="clone_boundary
clone_end:SP6
site:EcoRI"
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190. 1289
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295. 2710
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508. .2771
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rpt_family="L1MB3"
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REPERENCE 3 (bases 1 to 1182) AUTHORS Direct Submitted (109-AUG-2001) Biber K.P.H., Medical Physiology, State JOURNAL University Groningen, Ant. Deusinglaan 1, 9713 AV Groningen, NETHERLANDS FRATURES Location/Qualifiers 11182 Anti-Cross Anti-Cross	Query Match 99.44; Score 1076.6; DB 10; Length 1182; Best Local Similarity 99.64; Pred. No. 2.2e-289; Indels 0; Gaps 0; Best Local Similarity 99.64; Pred. No. 2.2e-289; Indels 0; Gaps 0; Argantachacachacaccacachantacharactacharathachacachachachachachachachachachachacha
Db 210399 AGCGAGGTGTTTTCCAACATCCTCCTTGTGCAAGGATACAGGGTGTTTTCCCAAGGG 210458 Oy 421 CGACTGGCCTCCATCTTCACACAGTGTTTTTGTGGTATTGTTGCGTCATCTGGCATGG 480 210459 CGACTGGCCTCCATCTTCACACAGTGTCTTGTGGTATTGTTGCGTGCATCTGGCATGG 210518 Oy 481 GCCATGGCCTCCATCTTTGCCCGAGTTTTTATGAGCCTCGGATGGAAGG 210518 Oy 541 CACAGGCTCACTTTGCCCAACAGTGTTTTTATGAGCCTCGGATGGAAGG 210518 Oy 541 CACAGCCGCTACTTTGCCCAACTTTTTTTTTTTTTTTTT	210939 CCGCTGCTTATTTGCTTCTTGACCGGAGGCCTTATGAGGATACCTTCGCGGCCTGTTC 500 [

61 CTGGACAACAGTGGGCCGGACCAACTTCCGCCCCGAGTTCCTCCCCCCAGCAGGTG 526 CTGGACAACAGTGGGCCGGACCAACTTCCCCCCCGAGTTCCTCCCCCCAGCAGGTG 121 CTGCAGTTCTGCTGCCCCGGTGTTTGCGGTGGATCCTTTGCACCAGCAGGTG 122 CTGCAGTTCTGCTGCCCCGGTTTTGCGGTGGATCCTTTGCACCAGCTGGTGGCGGTGTTT 123 CTGCAGTTCTGCTGCCCCGGTTTTGCGGTGGGTCTCTTGGACAACCTGCTGGCGGGTGTTT 124 CTTTCAAACCTGTGTTTCCTGCTTCCCGGTTTCTGCACACTTCCTAAACCTGGCG 125 ATCTTGGTGAATACAAGACTCAAGATTCTGGGCAACATTCCTAAACCTGGCA 126 GAAAGCCCTGGCACCAGAATTCTGGGGTAACTTCTAAACCTGGCA 127 CAAACCCTGGCACCAGAATTCTGCTGCTTCCCTCCACGCGCACCACGCAGAGTT 128 AGCGAGTGTTTTCCAACTTCTCCTCTTTGCCGTTCTTGCACCCACTCCTGCACCACGCACACGCACACGCACACGCACACGCACACGCACACGCACACGCACACGCACACGCACACGCACACGCACACACGCACACACGCA	12 13 10 10 10 11 15
1 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6	8 6 8 6 8 6 8 6 8
4 6 6 9 9 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ORGANISM Mus musculus Eukaryota; Metazaa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. AUTHORS TITLE TITLE Transgenic mice containing targeted gene disruptions Patent: WO 10203793-A 29 17-JAN-2002; Deltagen, Inc. (US) FRATURES Location/Qualifiers Location/Qualifiers 1. 2045 FRATURES Ouery Match Ouery Match Best Local Similarity 99.4%; Score 1076.6; DB 6; Length 2045; Best Local Similarity 99.4%; Pred. No. 2.2e-258; Matches 1079; Conservative 0; Mismatches 4; Indels 0; Gaps 0; Matches 1079; Conservative 0; Mismatches 4; Indels 0; Gaps 0; Autschell

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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                      805 AGGAGGTGTTTTCCAACATCCTCCTTGTGCAAGGATACAGGGTGTTTTCCCAAGGG
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1465 AAAGGTCATGGCAGGCCCATTGAACTGTACAGCAATTTGCATCAAAGGCAGGATATAATA
                                                                                      GCCATGGCTACTGGCTCTCTTTGCCCGAGTCTGTGTTTATGAGCCTCGGATGGAAAGA
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                                                                    CGACTGGCCTCCATCTTCACGACAGTGTCTTGTGGTATTGTTGCGTGCATCCTGGCATGG
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CVAFNGLILDNYLAVFILVKYKGLKUKIANIALSNLCELLELPEPAPHTRAHGES
PGNGTCKVLVGLHSGSGLYSBYFSNILLLVQGYRAPEGGFLASIFTTVSCGIVACVLAM
AMATALSLPESVFYEPRHERQKHKCAFGKPHFLPIBAPLMKYVLTSKMIILVLAFPLL
KSSYHLDASVQYDQTQVDHKPALVITGYFLLMMAPYNTVLFLSAFQEHLSLQDB
KSSYHLDASVQVTQLATTHCCVNPLLYLLLDRKAFMRYLFSGFQBHLSLQDB
QQAPPRKGHGRPIELYSNLHQRQDII"
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mRNA, complete
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                            Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Ramania; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Raman, M.A. and Dorf, M.E. Mus musculus E01 mRNA, complete cds Mus musculus E01 mRNA, complete cds L Unpublished (1997)
E 2 (bases 1 to 2045)
S Berman, M.A. and Dorf, M.E. Direct Submission
L Submitted (15-OCT-1997) Pathology, Harvard University Medical School, 200 Longwood Avenue, Boston, MA 02115-5701, USA
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                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="129/sv"
/db xref="taxon:10090"
/cell type="astrocytes; peritoneal exudate"
1. 2045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445. .1527
/gene="B01"
/codon start=1
/product="putative beta chemokine receptor"
/procein id="AAB86479.1"
/db_xref="G1:2623641"
                                 2045 bp mRNA linear putative beta chemokine receptor (E01)
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Pred. No. 2.2e-258;
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                                                                                                                                  Mus musculus (house mouse)
Mus musculus
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Best Local Similarity 99.6%;
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-CCT-2002) Human Genome Sequencing Center, Department Submitted (09-CCT-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 23, 2002 this sequence version replaced gi:21739980. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequenting reads assembled using ALlas (http://www.hgsc.bcm.rmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequence and whole genome shotgun sequence reads. Both and sequence and whole genome shotgun sequence only contigs will be indicated in the feature table.
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Rat Genome Sequencing Consortium.
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14678 GAAAGCCCGGGCAATGAAGTTCTTGTTGTTGACACTCCACTCCATGGGCTTGTAC 74619
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                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
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                Assembly program: Phrap; version 0.990329
Consensus quality: 166231 bases at least Q40
Consensus quality: 17402 bases at least Q30
Consensus quality: 174722 bases at least Q30
Estimated insert size: 190923; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CTGGACAACAGTGGGCCGGACCAAGTTCCGGCCCCCGAGTTCCTCTCCCCCCAGGAGGTG
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                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 231984;
                                                                                                                                                                                                                                                                                                                                                                                                       1 137707: contig of 137707 bp in length

7708 137807: gap of unknown length

7808 218965: contig of 81158 bp in length

8966 219065: gap of unknown length

9066 231984: contig of 12919 bp in length.

10.0cation/Qualifiers

1. 231984

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//mol type="genomic DNA"

//db_xrefe="taxon:10116"
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87.6%; Pred. No. 3.5e-199;
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GCESSHNLDRSTLITKIIATTHCCWNPLLAWGPYNIALFLSARNEHFSLH
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/chromosome="13"
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
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                          cccccccrcrattrgcrtccac---aaggccttraggagcratcrgcagccrgtrc
CGACTGGCCTCCATCTTCACGACAGTGTCTTGTGGTATTGTTGCGTGCATCCTGGCATGG
                                                                                        GCCATGGCTACTGCGCTCTTTTGCCCCGAGTCTGTGTTTTATGAGCCTCGGATGGAAAGA
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Sinkai, H. and Uenishi, H.
Direct Submissive State (03-SEP-2003) Hiroki Shinkai, STAFF-Institute, Submitted (03-SEP-2003) Hiroki Shinkai, STAFF-Institute, Research Devision; 446-1 Ippsizuka, Kamiyokoba, Tsukuba, 305-0854, Japan (E-mail:sinkai@gene.staff.or.jp, Tel:81-29-838-2337)
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/product="chemokine C-C motif receptor-like 2 isoform A"
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LFVVFCYVRRRRTLKFGERGYDLFKLVFTINVVFLLMWGPYNIALFLSAFNEHFSLH
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Pred. No. 3.2e-96;
0; Mismatches 379;
                                                                                                                                                                                                                               'note="transcript variant A"
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                                                                                                                                 102. .1314
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Best Local Similarity 64.2%;
Matches 695; Conservative
                                                       number=1
                                                                                                              'number=2
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Sus.
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Ibaraki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Analysis of genomic structure of porcine CC chemokine receptor genes and their expression
Unpublished

(Insert to 1314)

Shinkai, H. and Unsishi, H.

Direct Submission
Submitted (03-SEP-2003) Hiroki Shinkai, STAFF-Institute, Second Research Devision; 446-1 Ippaizuka, Kamiyokoba, Tsukuba, Ibarak 305-0854, Japan (B-mail:sinkai@gene.staff.or.jp, Tel:81-29-838-2190, Fax:81-29-838-2337)

Location/Qualifiers
                                                         TTCTGGAAGCACTTTCTGACCCTAAAGATGAACATTTTGGGATTTCTTTTGCCACTGTTT
                                                                                                              GTTTTTATAATCTGCTGCAGGCAACTGAGGAGAAGGCAGAGCTTCAGGGAGAGACAGTAC
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GAAAACCAGAAATACAAGTGTTTCTTTTGGCAGACCGCTCTTCCTACCAGCTGATGAGACA
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                                                                                                                                                                                                                                                                                                           AATATTGCACTTTTCCTGCTTTCAACGAACACTTCTCCCTGCATGGTTGTGAGAGC
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Sus scrofa CCRL2 mRNA for chemokine C-C motif receptor-like 2,
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
TTCTGGAAGCACTTTCTGACCCTAAAGATGAACATTTTTGGGATTTCTTTTGCCACTGTTT
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                                                                                                                                                                                                                                                                                                                          994 AATATIGCACITITCCIGICTITICAACGAACACTICICCCIGCAIGGITGIGAGAGC
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2 (bases 1 to 144233)
2 (bases 1 to 144233)
Shinkai,H. and Uenishi,H.
Direct Submission
Submitted (12-MAY-2003) Hiroki Shinkai, STAFF-Institute; 446-1
Ippaizuka, Kamiyokoba, Tsukuba, Ibaraki 305-0854, Japan
(E-mail:sinkai@gene.staff.or.jp, Tel:81-29-838-2190,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Uenishi,H.
Cloning of porcine CC chemokine receptor genes and clustering
structure on SSC13
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/organism="Sus scrofa"
/mol type="genomic DNA"
/db_Xref="taxon:9823"
/chromosone="13"
/map="13421"
/clone="0479G08"
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/gene="CCR3"
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118655 AATATTGCACTTTTCCTGTCTGCTTTCAACGAACACTTCTCCCTGCATGGTTGTGAGAGC 118714
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CQKTSVGQIEALLLPPLYSLVFIFGFVGNLLVVLILINCKKLKSMTDIYLLNLAISDL
LEPLFIPEWAHYAADOWFGNIMCKFFFGATHIGFFGATFILLFIDTAYLAIVHAVF
ALKARTTFGVVTSGYTSGYTSTATTSTATTATTSTATTATTAYNVN
RSILGLVLPLLVMVVCYSGILKTLLRCRNEKKGHKAVRLIFVIMIVYFLFWAPYNIVL
LLSTFQVFFGLSNCKNSSGLDQAMQVTETLGITHCCINPIIYAFVGEKFRRYLSVFFR
KHISKHCKQCPVFYGETGDRMSSTYTPSTGEQEVSAAL"
19514. .19519
/note="putative"
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Sus scrofa CC chemokine receptor genes (CCR2, CCR5, CCRL2, LTF,
TMEM7, LRRC2), complete cds, clone: 0475A03.
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Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                               2 [bases 1 to 165558]
Shinkai, H. and Uenishi, H.
Direct Submission
Submitted (27-JAN-2003) Hiroki Shinkai, STAFF-Institute; 446-1
Ippaizuka, Kamiyokoba, Tsukuba, Ibaraki 305-0854, Japan
(E-mail:sinkai@gene.staff.or.jp, Tel:81-29-838-2190,
                                                                                                                                    GTCAACCCGCTGCTCTATTTGCTTCTTGACCGGAAGGCCTTTATGAGATACCTTCGCAGC
                                                                                                                                                                                                                                                                                                                                        CTGTTCCCACGGTGCAATGATATCCCCTATCAAAGTAGTGGAGGCTATCAGCAAGCGCCT
                                                                1015 CCAAGGGAAGGTCATGGCAGGCCCATTGAACTGTACAGCAATTTGCATCAAAGGCAGGAT
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/protein_id="BAD08648.1"
/db_xrefe="GI:41688295"
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| Corganisme Sus scrofa | Mol_type="genomic DNA" | Mol_type="genomic DNA" | Mol_type="lagonaic DNA" | Moltanisme | Moltanisme DNA" | Moltanis
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AP006185,1 GI:41688294
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                                                                                                                                                                                                                                           translation="KGEADAMSLDGGFIYTAGKCGLVPVLAENQKSRQSSSSDCVHRP/
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       .139388,140524. .140571,142786. .>142876))
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                                                                   /note="reverse transcriptional orientation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.6%; Score 428.6; DB 4; Length 64.2%; Pred. No. 3.5e-96; tive 0; Mismatches 379; Indels
                                                                                                                                /product="lactotransferrin"
/protein_id="BAD08658.1"
/db_xref="GI:41688306"
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  /translation="mamgontevwkqvpqeliqevkpwhmwtlildrsllpnilkpgm
TQYQQWaFarrqcsscsqnwassqvqvlffhmwsegesrgqvkmrifsqrkkcsqss
FEVPKFTEBNISRILMNLJLRILKKCYGEGFRJUEIPITISYSLEGPHDSDNCEACLQ
FEVPKFTEBNISRILMNLJLRILKKCYGEGFRJUEIPITISHDSPHDSDNCEACLQ
FEVPKFTEBNISRILMNLJLRISPPVEIAIQPSPTRSSTTEDAVKKKVIPRPWF
PEATQAESLPTSWFRADTNSQNQRAIISSQGFRADTNSSQGRYDISSQNLPAKTNS
QSPRRKTNSQSPRAKTKGQSPRIDTSSQRFYKLPVTSQAHTGSTRLPSEFNA"
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EENNFVAECRRKGIPQAVYCKNGFVDTSVRLLDKIERNSLARQSSLSKEGHKWSSEFV
FELFGEHWWERPDSLKEQTHLKEWHISNTLIQIIPYIELPQAMRILDLPKNQISRLP
AEIGRLKNLKELNVSFNYLKSIPPELGOGCHLEKLDCSGNLELTELPFELSNLKQASF
VDLSANKFSSVPICYLRMSNLQWLDISNNNINDLPQDIDRLEELQTFLLYKNKLTYLP
YALLNLKKLTLLVVSGDHLVELPTALCDSSTPLKFISLMDNPIENTQCQDGDELVESE
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/protein_id="BAD08653.1"
/db_xref="GI:41688300"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="reverse transcriptional orientation"
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                                                                                                                                                                                                                                                      reverse transcriptional orientation"
complement join [129446. 129453, 130537.
133464. 13519, 135288. 135433, 13738.
144479. 144635, 149871. 150078, 155035.
                                                                                                                                                                                                                                                                                                                                                                       complement (join (129446. .129453,130537.
133464. .133619,135288. .135433,137338.
134479. .144635,149871. .150078,155035.
/genea"LRRC2"
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                                                                                                                                                   125401. .125406
/note="putative"
129140. .129145
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// Codon start=1
/ Codon start=1
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/ Product="lactotransferrin"
/ Product="lactotransferrin"
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GNAYYAAVAVVKKGFNFQLNQLGGSFOGOKDLFRDATTGFLK.FPSKIDSKLY
GUNSIWELLYQSQKKFGKSNPQEFQLFGSPGQNCDLFRDATTGFLK.FPSKIDSKLY
IGLPYLTALGCLRFTAARVBARQAKVWCAVGPFELRKCROWSSQSSQNLNCSLASTT
EDCIVQVLKGFADMSLDGGFTYTAACKGLVPVLAENQKSRQSSSSDCVHRPTGGYFA
VAVVRKANGGTTWNSVRGTYSCHTAAVDRAGNNIPMGLLVNQTGSCKFDFFFFR
GSQPGGNLCALCVGNDQGVDKCVPNNNERRYYGYTGARNGDNAFVKDYTVLDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="chemokine (G-C motif) receptor-like 2"
/protein id="BAD08650.1"
/db_xref="df::41688297"
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DPGEPLCKILLVLYSVGLFSEAFFNVLLTVQRYQKFPQMRGFFSATRMVAGSIFPSAL
NWTAVLYNMALPELAFYXRQMENQKYKCFFGRPLFLPADFTRNHFFLLIKWNIGFLLP
LPVFVFCYYMRRTLKFGERGYDLFKLVFTIMVVFLLMMGPYNIALFLSAFNBHFSLH
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                                                                                                                                                /trānslation="MDYQTT8PFYDIDYGMBEPCQKTNVRQIAARLLPPLYSLVFIFG
PVGNLLVVLILINGKKLKSNTDIYLLNLAISDLLPLFITPFWAHYAADQWVFGNTMCQ
FLTGFYFIGFFSGIPFIILLTIDRYLAIVHAVFALKRATVTFGVVTSGVTWVYAIFAS
FLTGFYFIGFFSGYFFFFFSSYSYFFWKNFQTLKNVILGLVLPLLVMVVCYSGIL
KTLARCHNEKKKHRYNTLIPAIMIVYFLFWAPYNIVLLLSTFQFFFGLNNCSGNRLD
QAMQVTETLGMTHCCINPIIYAFVGEKFRSYLLGFFRKHIVRRFCKGCPVFQAEAPDR
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complement (join (59868. 59902,61578. 61767,63435. .63619,
65539. .65606,65944. .70085,70628. .70783,71919. .71966,
74181. .74271,75721. .75875,76641. .76815,77275. .77453,
82891. .82946,83771. .83918,84248. .84430,84770. .84872,
/gene="LTF"
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VLLTEQAQFGRYGKDCPDKFCLFRSETKNLLFNDNTECLAQLQGKTTYEKYLGSEYVT
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/godon_gtart=1
/prod:..-
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/gene="TMEM7"
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/db_xref="G1:41688296"
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400te="putative"
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/note="putative"
59705. .59710
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other
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                                      Score 737.8; DB 5;
Pred. No. 6.3e-204;
0; Mismatches 22;
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al Similarity 96.5%;
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EST 25-JUL-2003

CF147784 11near 716 bp mRNA linear ES? AGENCOURT 14740191 NIH MGC 145 Homo sapiens cDNA clone IMAGE:6971947 5', mRNA sequence.

LOCUS

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E 1 (bases 1 to 716)

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH

Bidg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

CONA Library Arrayed by: The I.M.A.G.E. Consortium

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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ive 0; Mismatches 6;
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High quality sequence stop: 634.
Location/Qualifiers
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CF147784.1 GI:33244052
                                                                                         Homo sapiens (human)
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/organism="Homo sapiens"
/mol_type="MRNA"
/db xref="taxon:9606"
/clone="UI-H-FTI-bkc-j-11-0-UI"
/tisuue_type="Alveolar Macrophage"
/dev_stage="Alveolar Macrophage"
/dev_stage="Adult"
/lab host="DH10B (Life Technologies)"
/clone=lib="NCI CGAP_FTI"
/lone="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I;
NCI CGAP_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were outlured in some of the conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seg primer: Mi3 FORWARD
POLYA-Yes.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
GCCAGGAGGAGGGGCCCTGTGGCATCATTACAAGTGTCCTGGCATGGGTAACAGCCATT
                                                                                     GCCAGAGGAGGGTGCCTGTGGCATCATTACAAGTGTCCTGGCATGGGTAACAGCCATT
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UI-H-FT1-bkc-j-11-0-UI 3', mRNA sequence.
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CD370587/c
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hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; Rlebbiella moi 10, 3 hours; Rlebsiella moi 10, 24 hours; Klebbiella moi 10, 24 hours; Klebbiella moi 10, 24 hours; Klebbiella moi 10, 24 hours; Raph aureus moi 10, 24 hours; Adenoviral vector (Ads CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ads CMV eGFP), moi 500, 24 hours; Adenoviral vector (Ads CMV eGFP), moi 500, 24 hours; Ad edenovirus moi 500, 3 hours; At adenovirus H. LPS 3 hours; At adenovirus + LPS 24 hours; The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into py773-Pac vector. The oligonucleotide used to prime the synthesis of first-errand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. THE CHANNEL WALLEY CONTAINS THE CONTAINS 1030 430 432 372 312 850 910 192 970 672 490 612 550 552 610 551 GCAGAACTCCCTTCCTGCCAGCTGATGAGACATTCTGGAAGCATTTTCTGACTTTAAAAA 492 670 730 790 252 72 671 GGGTGCCCTGTGGCATCATTACAAGTGTCCTGGCATGGGTAACAGCCATTCTGGCACTT 491 TGCCTGAATTCGTGGTTTATAAACCTCAGATGGAAGACGAGAAATACAAGTGTGCATTTA GAAAAACACTAAGGTTCAGGGAGCAGAGGTATAGCCTTTTCAAGCTTGTTTTTGCCATAA 251 TCACTAAACTCATCGCCACCACCACTGCATCAACCCTCTCCTGTATGCGTTTCTTG 911 ATGGGACATTTAGCAAATACCTCTGCCGCTGTTTCCATCTGCGGTAGTAACACCCCACTTC 371 TGACTGTGCAAAGGTACCTAGTGTTTTTGCACAAGGGCAACTTTTTCTCAGCAGGAGGA 729 TGACTGTGCAAAGGTACCTAGTG-TTTTGCACAAGGGCAAC-TTTTCTCAGCCAGGAGGA 431 GGGTGCCCTGTGGCATCATTACAAGTGTCCTGGCATGGGTAACAGCCATTCTGGCCACTT 611 TGCCTGAATACGTGGTTTATAAACCTCAGATGGAAGACCAGAAATACAAGTGTGCATTTA GCAGAACTCCCTTCCTGCCAGCTGATGAGACATTTCTGGAAGCATTTTCTGACTTTTAAAAA TGAACATTTCGGTTCTTGTCCTCCCCCTATTTATTTTACATTTCTCTATGTGCAAATGA GAAAAACACTAAGGTTCAGGGAGCAGAGGTATAGCCTTTTCAAGCTTGTTTTTGCCGTAA TGGTAGTCTTCCTTCTGATGTGGGCGCCCTACAATATTGCATTTTTCCTGTCCACTTTCA 791 AAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTGGACAAAAGTGTTCACA 311 AAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTGGACAAAAGTGTTCACA TCACTAAACTCATCGCCACCCACCCACTGCTGCATCAACCCTCCTGTATGCGTTTCTTG Gapa 7 Query Match 61.6%; Score 637.8; DB 6; Length 729; Best Local Similarity 99.4%; Pred. No. 1e-174; Matches 661; Conservative 0; Mismatches 2; Indels 2. TAG_TISSUE=Human Lung Alveolar Macrophage TAG_LIB=UI-H-FT1

LOCUS DEFINITION

CD520843

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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B1834559 831 bp mRNA linear EST 04-OCT-2001
603089767F1 NIH_MGC_120 Homo saplens CDNA clone IMAGE:5228561 5',
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/clone="thAGE:5228561"
/lab host="DH10B"
/clone lib="NIH_MGC 120"
/note="Cycgan: pooled pancreas and spleen; Vector:
pCWV-SPORT6; Site 1: Not1; Site 2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo
                                                                                                                                              300
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185 GIGCCATCACTCTGCTCTGCTGTTTTGTGATCGGTGTCCTGGACAATCTCCTGGTTGTG 244
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Catarrhini, Hominidae, Homo.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
                                                                       241 GCAGTTTCTAACTTGTGTTTTCTTGCCTGCCCTTCTGGGCTCATGCTGGGGGGAT
                                                                                                                                                                                                                                                                                               365 CCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTACAGTGAGACATTTTTC
                                                                                                                                                                                                                                                                                                                                          361 AATTGCCTTCTGACTGTGCAAAGGTACCTAGTGTTTTTGCACAAGGGCAACTTTTTCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 CTGGCCACTTTGCCTGAATTCGTGGTTTATAAACCTCAGATGGAAGACCAGAAATACAAG
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1 (Dases 1 to 831)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601 ACTITAAAAATGAACATITCGGTTCTTGTCCTCCCCCTAITTATITT 648
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/organism="Homo sapiens"
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Homo sapiens
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/lab host="Pooled"
/lab host="Pooled"
/lab host="Pooled"
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/clone lib="Whi MGC 1919."
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Site 2: Sfil (ggcgcctcggcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn loncowcin. 5' adaptor sequence:
5'-CAGGCCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCAGGCCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCAGGCCGAGGGCGCGACATG-dT (30) BN-3' (where B = A, C, Or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
                                                                                                                                              720 bp mRNA linear EST 06-JUN-2003
AGENCOURT 14369985 NIH MGC 191 Homo sapiens CDNA clone
IMAGE:30400698 5', mRNA sequence.
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1 (basea 1 to 720)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genemics / NIH
Diffice of Cancer Genemics / NIH
Bldg. 31 Rml0A07 Betheda, MD 20892
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.k column: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 497.
Location/Qualifiers
                                                                                                                                                                                                                                                                          CD520843.1 GI:31452561
                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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       TGTAA 1035
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/tissue_type="mixed"
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/lab_host="mixed"
/clone_lib="NIH_MGC_lab"
/clone_lib="NIH_MGC_lab"
/note="Vector: pcoRN3.1; Site 1: multiple; Site 2:
/note="Vector: pcoRN3.1; Site 1: multiple; Site 2:
multiple; ORF's were PCR-amplffied (from IMAGE clones or
from commercially available cDNA libearies) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pcoNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
ftp://inage.lnl.gov.image.rearrayed_plates/IRBF.preSV.dat
a. Note: this is a NIH_MGC Library."
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A70 Betheada, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov a column: 08
High quality sequence start: 18
High quality sequence start: 18
High quality sequence stop: 630.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.4%; Score 594.4; DB 7; Length 773; 98.2%; Pred. No. 5.1e-162; Live 0; Mismatches 10; Indels 1;
                                                                                                                                                                                                                                                                                                          1. .773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 98.2
Matches 610; Conservative
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male. Library is oligo-dT primed and directionally cloned (EcoRV afte is destroyed upon cloning). Average insert size 1.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
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NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                      GAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCCAGGCACTCTCAGCCCAGCTG
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                                                                                                                                                    Query Match 58.9%; Score 609.8; DB 4; Best Local Similarity 99.4%; Pred. No. 1.6e-166; Matches 633; Conservative 0; Mismatches 2;
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BE871331 750 bp mRNA linear EST 20-OCT-2000 601449442F1 NIH_MGC_65 Home sapiens cDNA clone IMAGE:3853378 5',
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/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC_65"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
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                                                   479 GCAGTITCTAACTIGIGITTCTTGCTTACCCTGCCCTTCTGGGCTCATGCTGGGGGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 CCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTACAGTGAGACATTTTTC
                                                                                                                                                                                                                                                                         361 AATTGCCTTCTGACTGTGCAAAGGTACCTAGTGTTTTTGCACAAGGGCAACTTTTTCTCA
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(Dases 1 to 880)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
158 CCTGTATGCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGTTTCCATCTGCG 99
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                                                                                   98 TAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACAAGGCACATCGAGGGAAGAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapBs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can bettp://image.llnl.gov
http://image.llnl.gov
Plate: LLAMI1454 row: b column: 23
High quality sequence stop: 809.
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/db_xref="taxon:9606"
/clone="IMAGE:5182006"
/lab_host="bH108"
/clone_lib="NIH_MGC_115"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/tissue types="blood"
/cell types="blood"
/cell types="leukcytes"
/lab host="bliod"
/coll types="leukcytes"
/lab host="bliod"
/clone lib="Stimulated peripheral blood leukcytes S3"
/clone lib="Stimulated peripheral blood leukcytes S3"
/notes="Organ: circulatory system, Vector: pME188-FL3;
Site l: Xhol; Site 2: Xhol; The library was prepared from polyh- RNA from equine peripheral blood leukcytes were solated from a healthy adult horse. The leukcytes were stimulated for 4 hr with 10 ng/ml E. coli O55:B5 LPS.
Double-stranded cDNA was cloned unidirectionally into different brail sites of the pME188-FL3 vector (5-prime Drall site is CACCATGTCTG, 3-prime Drall site is
CACCATGTCT). Xhol excises the cDNA insert."
            Library constructed by Dr. Yutaka Suzuki and Dr. Sumlo Sugano in the Human Genome Center. University of Tokyo Institute of Medical Science: tissue and RNA were prepared in the Department of Large Animal Medicine, University of Georgia; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia; Sequence ends have been trimmed to exclude vector and regions Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Seq primer: Sug3 (CGACCTGCAGCACA)
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                                                                                                                                                                                                                                                 /organism="Equus caballus"
/mol_type="mRNA"
/strain="Tennesee walking horse"
                                                                                                                                                                                                                                                                                                      db xref="taxon:9796"
/clone="LeukoS3_3_F11_A025"
/sex="female"
                                                                                                                                                                                                              location/Qualifiers
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( Dases 1 to 768)

Vandenplas, M., Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Moore, J.N., Liang, C., Sun, F., Sullivan, R., Shah, M. and Pratt, L.H. An EST database from equine (Equus caballus) stimulated peripheral blood leukocytes.
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                                                                                                                                                        ATGGCCAATTACACGCTGGCACCAGAGGATGAATATGATGTCCTCATAGAAGGTGAACTG
                                                                                                                                                                                                                               GAGAGCGATGAGCAGAGCAATGTGAAAGAATGAGGCCCCAGGCACTCTCAGCCCAGCTG
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Other ESTS: LeukoS3 3 F11.g1 A025
Contact: Cordonnier-Pratt MM—
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
                                                                                             3.
                                                    Length 750;
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                                                      Score 470.2; DB 2;
Pred. No. 1e-125;
0; Mismatches 23;
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Equus caballus
                                                    Query Match
Best Local Similarity 95.2%;
Matches 517; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

I (bases 1 to 736)
Vandenplas, M., Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S.,
Moore, J.N., Liang, C., Sun, P., Sullivan, R., Shah, M. and Pratt, L.H.
An EST database from equine (Equus caballus) unstimulated
peripheral blood leukocytes
Unpublished (2003)
Other ESTs: LeukoN2_2_B11.g1_A024
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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LeukoN2_2_B11.b1 A024 Unstimulated peripheral blood leukocytes N2
Equus caballus cDNA clone LeukoN2_2_B11_A024 3', mRNA sequence.
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300 GAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCCAGGCACTCTCAGCCCCAGGCTG 359
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720 TTCTTGCCCACTTTGCCTGAATTCGGTGGTTATAAGC 756
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/strain="thoroughbred"
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Fax: 706 583 0210
Email: mmpratt@uga.edu
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60245580F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4584043 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="adenocarcinoma cell line"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lone_line="NIH_MGC_15"
/note="Organ: Golon; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by Oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGGAGGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using 2AP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
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                                                              61 GAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCCAGGCACTCTCAGCCCAGCTG 120
                                                                                                                                      TGTATGCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGTTTCCATCTGCGTA 955
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1309 row: o column: 20
High quality sequence stop: 626.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1035)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mcr.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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41.8%; Score 433; DB 4; Length 1035;
Best Local Similarity 93.6%; Pred. No. 8.8e-115;
Matches 484; Conservative 0; Mismatches 30; Indels
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/clone="IMAGE:4584043"
                                                                                                                                                                                                                                                                                                                                                      1016 ACCATTCCACCGAAGTGTAA 1035
                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
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BG386374
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Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810047105 product:chemokine (C-C) receptor 1,-like 2, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2111)
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                                                                                                                                                                                                                                  Chordata, Craniata, Vertebrata, Euteleostomi,
Rodentia; Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraties for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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                                                                                                                                                                                                                                                                                                                         Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Weth. Enzymol. 303, 19-44 (1999)
99279253
                                                                                                            AK007808.1 GI:12841594
HTC; CAP trapper.
Mus musculus (house mouse)
                                                                                                                                                                                                                                        Eukaryota, Metazoa;
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                                                                    /call type="blood"
/call type="blood"
/call type="leukocytes"
/lab host="bH108-TI phage-resistant E. coli"
/lab host="bH108-TI phage-resistant E. coli"
/clone lib="Unstimulated peripheral blood leukocytes N2"
/clone lib="Unstimulated peripheral phood leukocytes isolated from the library was prepared from polyA+ RNA from unstimulated equine peripheral blood leukocytes isolated from a healthy adult horse.
Double-stranded cDNA was cloned unidirectionally into different brailI sites of the pME185-FL3 vector (5-prime DraIII site is CACCATGTG, 3-prime DraIII site is CACCATGTG, 3-prime DraIII site is CACCATGTG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 421.6; DB 6; Length 736;
Pred. No. 1.7e-111;
0; Mismatches 144; Indels 15;
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cal Similarity 77.4%;
543; Conservative
                                                 sex="male"
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Eukaryota; Butheria; Perissodactyla; Equidae; Equus.

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S vandemplas, M., Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S.,
Moore, J.N., Liang, C., Sun, F., Sullivan, R., Shah, M. and Pratt, L.H.
An EST database from equine (Equus caballus) unstimulated
peripheral blood leukocytes
Unpublished (2003)
Other ESTs: Leukonz 4 E11. bl. A024
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 583 0210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="unnamed protein product; chemokine (C-C) receptor 1,-like 2 (MGD|MGI:1920904, GB|NM_017466, evidence: BLASTN, 98*, match=2039)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGACAACAGTGGGCCGGACCAAGTT-----CCGGCCCCCGAGTTCCTCTCCCCCCAG
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larity 65.7%; Pred. No. 4.1e-109;
Conservative 0; Mismatches 330; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |db_xref="FANTOM_DB:1810047105"
|db_xref="taxon:10090"
|clone="1810047105"
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/mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                  643 ATTITITACATTICTCTATGTGCAAATGAGAAAAACACTAAGGTTCAGGGAGCAGAGGTAT 702
        662 TTCTGGAAGCATTTTCTGACCTTGAGGACGAACATTTTTGGACTTCTTTTCCCACTGTTT
                                                                                                                                                                                                                                                                                                                                                 GITITITATATITIGCTATGIGCGAATGAG-AAAACAATAAGATTIGGGAAAAGGAGATAT
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AGENCOURT 30842774 NIH_MGC_146 Homo sapiens cDNA clone
IMAGE:7389718 5', mRNA sequence.
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98.5%; Pred. No. 1.1e-102;
iive 0; Mismatches 6;
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C0959203.1 GI:51323783
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Matches 395; Conserv
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KEYWORDS
SOURCE
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AUTHORS
TITLE
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COMMENT
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CO959203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Justice Lype="blood"
/ Lissue Lype="blood"
/ Cell type="leukocytes"
/ Lell type="leukocytes"
/ Lell type="leukocytes"
/ Lell type="Union-riphage-resistant E. coli"
/ Clone lib="Unstimulated peripheral blood leukocytes N2"
/ Note="Organ: circulatory system; Vector: pWE18S-FL3;
Site 1: Xhol; Site 2: Xhol; The library was prepared from polyA+ RNA from unstimulated equine peripheral blood leukocytes isolated from a healthy adult horse.
Double-stranded cDNA was cloned unidirectionally into different Draili sites of the pME18S-FL3 vector (5-prime Draili site is CACCATGTG, 3-prime Draili site is CACCATGTG; Xhol excises the cDNA insert."
Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center. University of Tokyo Institute of Medical
Science; tissue and RNA were prepared in the Department of Large
Animal Medicalne, University of Georgia; sequencing done in the
Laboratory for Genomics and Bioinformatics, University of Georgia.
Sequence ends have been trimmed to exclude vector and regions below
Phred quality 16. Three-prime sequences are presented as their
reverse complement and have been trimmed to exclude polyA.
Seq primer: Sugs (CTTCTGCTCTAAAAAGCTGCG).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 ATGGCTAATTACACGTCCACACCAGAGGATGATATGATGTCCTCATAGAGGACGATCTG 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGGCCAACTITITCTCAGCCAGGAGGAGGGTGCCCTGTGGCATCATTACAAGTGTCCTG 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .789
/organisms="Equus caballus"
/mol_type="mRNA"
/furains=thoroughbred"
/db_xref="taxon:9796"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="LeukoN2_4_E11_A024"
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1 (Dasses I to 683)

8 Vandemplas, M., Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Moore, J.N., Liang, C., Sun, F., Sullivan, R., Shah, M. and Pratt, L.H. An EST database from equine (Equus caballus) unstimulated peripheral blood leukocytes

1 Unpublished (2003)

Other ESTs: LeukoNS 3 C06.91 A027

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeukoNS_3_C06.bl_A027 Unstimulated peripheral blood leukocytes NS
Equus caballus cDNA clone LeukoNS_3_C06_A027 3', mRNA sequence.
CDS35056.1 GI:31577471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 70s 383 0210

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in

the Human Genome Center, University of Tokyo Institute of Medical

Science, tissue and RNA were prepared in the Department of Large

Animal Medicine, University of Georgia; sequencing done in the

Laboratory for Genomics and Bloinformatics, University of Georgia.

Sequence ends have been trimmed to exclude vector and regions below

Phred quality 16. Three-prime sequences are presented as their

reverse complement and have been trimmed to exclude polyA.

Seq primer: Sug3 (CGACCTGCAGCACA)
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                                   120
                                                                                                                                                   182
                                                                                                                                                                                                                                                                 CCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTACAGTGAGACACTTTTTC 362
                                     GAGAGCGATGAGCCAGAGCAATGTGACAAGTATGACGCCCAGGCACTCTCAGCCCAGCTG
                                                          GAGAGCGATGAGCAGAACAATGTGACAAGTATGACGCCCCAGGCACTCTCAGCCCCAGCTG
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ATGGCCAATTACACGCTGGCACCAGAGGAAGAATATGATGTCCTCATAGAAGGTGAACTG
                                                                                                             GTGCCATCACTCTGCTCTGCTGTTTGTGATCGGTGTCCTGGACAATCTCCTGGTTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Equus caballus"
/mol_type="mRNA"
/strain="Dartmoor Pony"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="blood"
/cell_type="leukocytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9796"
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Equus caballus
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1030
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Unstimulated peripheral blood leukocytes NS"
/clone_lib="Unstimulated peripheral blood leukocytes NS"
/note="Organ: circulatory system; Vector: pWE18S-FL3;
Site_1: XhoI; Site_2: XhoI; The library was prepared from polyA+ RNA from unstimulated equina peripheral blood leukocytes isolated from a healthy adult horse.
Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pWE18S-FL3 vector (5-prime DraIII site as CACTGTCTG, 3-prime DraIII site is CACTGTCTG; 3-prime DraIII site is
                                                                                                                                                                                                                                                                                                                                                                                       7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       731 TGGTAGICTTCCTICTGATGTGGGCGCCCTACAATATTGCATTTTTCCTGTCCACTTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 AAGACTACTICTGCCTGCAAGACTGCAGGCACGCTACAACCTGGACAAAAGTGTTCACA
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                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                              Query Match 37.6%; Score 389.4; DB 6; Best Local Similarity 76.5%; Pred. No. 4.2e-102; Matches 509; Conservative 0; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              completed: June 18, 2005, 12:07:55
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Sequence 3, Appli Sequence 1085, Ap Sequence 905, App Sequence 959, App Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 15, Appli Sequence 1, Appli Sequence 1011, Appli Sequence 1011, Appli Sequence 1011, Appli Sequence 1, Appli

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GTGCCATCACTCTGCTCTGCTGTGTTTGTGATCGGTGTCCTGGACAATCTCCTGGTTGT 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 ATGGCCAATTACACGCTGGCACCAGAGGATGAATATGATGTCCTCATAGAAGGTGAACTG
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Sequence 11, Application US/10039659A

GENERAL INFORMATION:
APPLICANT: Glah, Kurt C.
APPLICANT: Glah, Kurt C.
APPLICANT: Schall, Thomas J.
APPLICANT: Schall, Thomas J.
APPLICANT: Invertion Antibodies that bind chemokine TECK
TITLE OF INVENTION: Antibodies that bind chemokine TECK
FILE REFERENCE: DXOS99XIB US
CURRENT APPLICATION NUMBER: US/10/039,659A

CURRENT APPLICATION NUMBER: US 08/887,977

PRIOR APPLICATION NUMBER: US 60/021,664

PRIOR PILING DATE: 1996-07-03

PRIOR FILING DATE: 1996-07-03

PRIOR FILING DATE: 1996-10-11

PRIOR FILING DATE: 1996-10-11

PRIOR FILING DATE: 1997-06-04

NUMBER OF SEQ ID NOS: 26

SOFTUMBER: PALENTIN VERSION 3.1
US-08-375-199B-3

US-09-720-565-3

US-09-016-514-1085

US-09-023-655-959

US-08-575-957A-3

US-08-771-776-3

US-08-771-776-3

US-08-771-776-3

US-08-771-776-3

US-09-826-509-474

US-09-931-3381A-15

US-09-931-39B-1

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100.0%; Score 1035;
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Matches 1035; Conservative 0; Mismatches
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LENGTH: 1547
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                                                                                                                                                                                                                                                                                           June 18, 2005, 06:41:10 ; Search time 198.888 Seconds (without alignments) 8515.071 Million cell updates/sec
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6: /cgn2_6/ptodatea1/ina/PcTUS_COMB.seq:*

6: /cgn2_6/ptodatea1/ina/PcTUS_COMB.seq:*
                                                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-016-144-756

US-08-681-121

US-09-023-655-308

US-09-17-665-8

US-08-771-665-8

US-09-17-665-8

US-09-17-665-8

US-09-17-665-8

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US-09-13-655-951

US-09-13-655-951

US-09-13-655-951

US-09-13-170-3

US-09-13-170-3

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                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BM PC COMPALIDE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
99.5%; Score 1029.8;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1031; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
ATTORNEY, AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELECHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 756:
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 base pairs
STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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| IMMEDIATE SOURCE:
| LIBRARY: MPHGNOT03
| CLONE: 442279
| US-09-016-434-756
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| Patent No. 6500938
| GENERAL INFORMATION:
| APPLICANT: Janice Au-Young APPLICANT: Jeffrey J. Sellhamer
| TITLE OF INVENTION: PATHWAY GENE EXPRESSION
| TITLE OF SEQUENCES: 1490
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCACCGAAGTGTAA 1035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 973.4; DB 3;
Pred. No. 1.3e-309;
0; Mismatches 1;
REFERENCE/DOCKET NUMBER: ATGS
TELECOMMUNICATION INFORMATION:
TELEFAM: 610-270-5031
TELEFAM: 610-270-4026
TELEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.99
Matches 974; Conservative
                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                ; ORIGINAL SC
US-08-681-192-1
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                                                                                TGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTCTGGAAGCATTTTCTG
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Sequence 1, Application US/08681192;
GENERAL INFORMATION;
APPLICANT: BERGSMA, DERK
APPLICANT: ELSGWA, HENRY
APPLICANT: RUBEN, STEVEN
ITILE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNFDS78
ITILE OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEB: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
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ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMFUTER: Diskette
COMFUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PRACENO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,192
FILING DATE:
CLASSIPFCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
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NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
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Sequence 8, Application US/09517605

Patent No. 6391567

GRERRAL INPORMATION:
APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: Gaitenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: US/09/517,605
CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT PILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
ILENGTH: 1059
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                                                                                                                         65 TGCATTTTTCCTGTCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTA 124
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                                                                           768 TGCATTTTTCCTGTCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTA
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                                                                               856 TCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTGGACAAA 915
                                                                                                                                                                                                                           AGTGTTCACATCACTAAACTCATCGCCACCCACTCGCTGCTGAACCCTCTCCTGTAT 975
                                                                                                                                                                                                                                                                                                                          GCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGTTTCCATCTGCGTAGTAAC 960
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Patent No. 6607879

GENERAL INFORMATION:
GENERAL INCORPATION:
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: EXPRESSION
ITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCTTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                      841 AGTGTTCACATCACTAAACTCATCGCCACCACCCACTGCTGCATCAACCCTCTCTGTAT
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Pred. No. 1.1e-96;
0; Mismatches 1; Indels 0
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MEDIUM TYPE: B4304

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER: IBM PC compatible

OPERATING EXSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURSINIA APPLICATION DATA:

APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH

CLASSIPICATION:

PRIOR PAPLICATION:

PRIOR DATA:

FILING DATA:

APPLICATION NUMBER:

FILING DATA:

APPLICATION NUMBER:

FILING DATA:

APPLICATION NUMBER:

FILING DATA:

ATTORNEY/AGENT INFORMATION:

NAMM: Zeller, Karen J.

REGISTRATION NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 845-0456

INFORMATION FOR SEQ ID NO: 308:

SEQUENCE CHARACTERICATICS:

LEMETRALE CAPACTERICATICS:

LEMETRALE CAPACTERICATICS:
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ilarity 99.7%;
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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; CLONE: 1378524
US-09-023-655-308
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STATE: CALIFORNIA
COUNTRY: USA
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Best Local Similarity
Matches 327; Conserva
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US-08-771-276-19
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TITICACAAGGCAACITITICICAGCCAGGAGGAGGGIGCCCIGIGGCAICATTACAAG 455
                              CGTCCATGCTGTGTTTTAAAAGCC---AGGACGGTCACCTTTGGGGTAGTGACAAG 446
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                                                             TGTCCTGGCATGGGTAACAGCCATTCTGGCCACTTTGCCTGAATTCGTGGTTTATAAACC
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Patent No. 6797811
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
SCHWeickart, Vicky L.
APPLICANT:
RAPORT, Carol J.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE:
ADDRESSEE:
ADDRESSEE:
GIOO Sears Tower, 233 S. Wacker Drive
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: No. 6797811and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33670
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Illinois
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US-08-771-276-19
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Pred. No. 9.6e-66;
0; Mismatches 365; Indels
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56.8%;
INFORMATION FOR SEQ ID NO: 19
SEQUENCE CHARACTERISTICS:
LENGTH: 1059 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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Matches 531; Conservative
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946
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---ATCCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTACAGTGAGACAT 355
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                                                                                             356 TITICAATIGCCTICTGACTGTGCAAAGGTACCTAGTGTTTTTGCACAAGGGCAACTTTT
                                                                                                                                              350 retricarectectedanicaraceracidesergiceretesicarecteri
                                                                                                                                                                                                                                                                                            476 CCATTCTGGCCACTTTGCCTGAATTCGTGGTTATAAACCTCAGATGGAAGACCAGAAAT
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                                                                                                                                                                                                                                                                                                                                                                                            536 ACAAGIGIGCATITAGCAGAACTCCCTTCCTGCCAGCTGATGAGCATTCTGGAAGCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     656 TCTATGTGCAAATGAGAAAAACACTA-----AGGTTCAGGGAGCAGGTATAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is Sequence 967, Application US/09023655
; Sequence 967, Application US/09023655
; Patent No. 6607879;
; APPLICANT: Cocks, Benjamin G.
APPLICANT: Jeffrey J. Seilhamer;
; APPLICANT: Jeffrey J. Seilhamer;
; APPLICANT: Jeffrey J. Seilhamer;
; TITLE OF INVENTION: COMPOSITION FOR THE DE
; TITLE OF INVENTION: 1508
CORRESPONDENCE ADDRESS:
ADDRESSES: 1807TE PHARMACEUTICALS, INC.
STREET: 3174 FORTER DRIVE
CITY: PALO ALTO
STREET: USA
ZIP: COUNTRY: USA
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                             Sequence 3, Application US/08724984A
Patent No. 6388055
GENERAL INFORMATION:
APPLICANT: DETK BETSHMA, MARY Brawner, and Usman Shabon
TITLE OF INVENTION: No. 6388055el Mouse Genomic Clone of the
TITLE OF INVENTION: CRRS Receptor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.3%; Score 230.6; DB 3; Length 1
57.0%; Pred. No. 6e-65;
tive 0; Mismatches 354; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                              918 CTACCTCTTAGTCTTCCAAAAGCACATTGCCA 952
                                                                                                  927 ATACCICIGCGCIGITICCATCTGCGTAGTAACA 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WINDOWS FOR WORKGROUPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: LILLING COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROU SOFTWARE: IBM 486
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/724,984A
FILING DATE: October 3, 1996
CLASSIFTATION: 800
PRIOR APPLICATION DATA: APPLICATION NUMBER: PLING DATE: APPLICATION NUMBER: ATTORNEY/AGENT INFORMATION:
NAME: William T. Han 34,344
REGISTRANCE/DOCKET NUMBER: AT55023
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SOUTH SOUTH SECTION OF STANDENS: 610 270 5090
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 1059
TYPE: NUCLEIC Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: NO
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                          RESULT 7
US-08-724-984A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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US-09-087-232A-12

| Sequence 12, Application US/09087232A
| Patent No. 6153431
| Patent No. 6153431
| GENERAL INFORMATION:
| APPLICANT: Quillent et al.
| TITLE OF INVENTION: HUMAN IMMUNOBERICIENCY VIRUS CO-RECEPTOR
| TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
| NUMBER OF SEQUENCES: 23
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                            784 Trigrecificicida Acadecifica de la refrancia de la refrancia de 13 de 13 de 14 de 14 de 15 d
                                                                                                                                                                                                                                                                                                                                                                                                             887 ACCCTCTCCTGTATGCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGTTTCC 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 CAGAGCAATGTGACAAGTATGACGCCCAGGCACTCTCAGCCCAGCTGGTGCCATCACTCT 133
                                                                                              724 CTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACA
                                                                                                                                                                                    TTGCATTTTTCCTGTCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCT
                                                                                                                                                                                                                                                                                                                                                       ACAATCTGGACAAAAGTGTTCACATCACTAAACTCATCGCCACCACCACTGCTGCATCA
         707 TITICAAGCITGITITIGCCGIAATGGIAGICTTCCTTCTGATGTGGGCGCCCCTACAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PERENTIN RELEASE #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 MAY 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
ATTORNEY AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: AP 31115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Baker & Botts, L.L.P. attn. Lisa Kole STREET: 30 Rockefeller Plaza CITY: New York CITY: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 230.6; DB 3;
Pred. No. 7.2e-65;
0; Mismatches 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 408-2628
TELEPAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 1376 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION TELEPHONE: (212) 408-2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 57.0
Matches 522; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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LOCATION: 240..1298
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         US/09/023,655
                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTATION UNDHER: 37,071
REFERENCE/DOCKET UNDHER: PA-OF
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAM: (650) 845-4166
INFORMATION FOR SEQ ID NO: 967:
SEQUENCE CHARACTERISTICS:
LENGTH: 1225 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER: US/
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
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; CLONE: 91502408
US-09-023-655-967
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Best Local Similarity
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                                                                                                                                                                                                                                               ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDIE
COMPUTER: IBM PC COMPALIDIE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION NUMBER:
PRIOR APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
NAME: Zeller, Karen J.
NEGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMINICATION INFORMATION:
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1104:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1376 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CLONE: 91262810
US-09-016-434-1104
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                                                                                                                     134 GCTCTGCTGTTTGTGATCGGTGTCCTGGACAATCTCCTGGTTGTGCTTATCCTGGTAA 193
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Sequence 1104, Application US/09016434

Patent No. 650039

GENERAL INFORMATION:

APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Sellhamer

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

TITLE OP INVENTION: PATHWAY GENE EXPRESSION
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Sequence 1, Application US/09502783A

Patent No. 6511826

GENERAL INFORMATION:
APPLICANT: 11, Y1
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: HOGNRIO
TITLE OF INVENTION: HOGNRIO
TITLE OF INVENTION: HOGNRIO
TITLE REPERENCE: 1488.115006
CURRENT APPLICATION NUMBER: US/09/502,783A
CURRENT APPLICATION NUMBER: US/09/66,343
PRIOR PILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patent In version 3.0
SEQ ID NO 1
LENGTH: 1414
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LOCATION: (259)..(1314)
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CTGTGTTTGCGTCTCTCCCAGGAATCATCTTTACCAGATCTCCAAAAAGAAGGTCTTCATT 765
                                                                                                                                                                                              CAGAGCAATGTGACAAGTATGACGCCCAGGCACTCTCAGCCCAGCTGCCCATCACTCT 133
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Patent No. 6548636
GENERAL INPORMATION:
APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCRS PEPTIDES FOR HIV-1 INFECTION
FILE REPERENCE: 2048/61010/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 11376
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Pred. No. 7.2e-65;
0; Mismatches 354; Indels 39;
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US-09-796-202-2
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Sequence 1, Application US/09502784A Patent No. 6743594 GENERAL INFORMATION:
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                                                                                                                                                       Gaps
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                                                                               Query Match 22.3%; Score 230.6; DB 4; Length 1414; Best Local Similarity 57.0%; Pred. No. 7.3e-65; Matches 522; Conservative 0; Mismatches 354; Indels 39;
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APPLICANT: Li, Yi
APPLICANT: Li, Yi
TITLE OF INVENTION: Methods of Screening Using Human G-Protein
TITLE OF INVENTION: Methods of Screening Using Human G-Protein
TITLE REFERENCE: 1468.1150005
FILE REFERENCE: 1468.1150005
CURRENT APPLICATION NUMBER: US/09/502,784A
CURRENT APPLICATION NUMBER: 09/195,662
PRIOR FILING DATE: 1998-11-18
PRIOR PRICK APPLICATION NUMBER: 08/466,343
PRIOR PRICK SEQ ID NOS: 9
SCOTWARE: Patentin Version 3.1
SEQ ID NO 1 39; Length 1414; Indels Query Match 22.3%; Score 230.6; DB 4; Best Local Similarity 57.0%; Pred. No. 7.3e-65; Matches 522; Conservative 0; Mismatches 354; 959 ò 셤

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Sequence 1. Application US/09195662A

| Sequence 1. Application US/09195662A
| Patent No. 6800729
| GENERAL INFORMATION:
| APPLICANT: Li, Yi
| APPLICANT: REPERRINCE: 1488.115002
| TITLE OF INVENTION: Human G-Protein Chemokine Receptor HDGNR10 (CCRS Receptor)
| FILE REPERRINCE: 1488.115002
| CURRENT APPLICATION NUMBER: 05/99/195,662A
| CURRENT FILING DATE: 1998-11-18
| PRIOR PILING DATE: 1998-06-06
| NUMBER OF SEQ ID NOS: 9
| SOFTWARE: PatentIn version 3.0
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                                                                       TCTCAGCCAGGAGGAGGGTGCCCTGTGGCATTACAAGTGTCCTGGCATGGGTAACAG 475
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OTHER INFORMATION: Description of Artifical Sequence: Genomic
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Best Local Similarity
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NAME/KEY: CDS
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i OTHER INFORMATION: Description of Artifical Sequence: Genomic US-09-339-912A-1
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ORGANISM: Artificial Sequence: Genomic
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Search completed: June 18, 2005, 12:14:47 Job time : 203.888 secs

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SEQ ID NO 31
LENGTH: 1035
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         June 18, 2005, 09:53:05; Search time 722.252 Seconds (without alignments) 8895.522 Million cell updates/sec
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Sequence 11,
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                                                                                                                                                                                                                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                                                                                                                     6054689 seqs, 3103772919 residues
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Maximum Match 100%
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Sequence 13, Appl Sequence 17557, A

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US-10-039-659-11 US-10-754-071-11 US-10-759-860-11 US-10-741-600-12 US-10-741-600-13 US-10-741-600-13

100.0 100.0 100.0 99.7 99.7

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APPLICANT: RIJKBULIVE Estit H.W.G.M.
APPLICANT: Boddeke, Erik H.W.G.M.
APPLICANT: Boddeke, Erik H.W.G.M.
APPLICANT: Boddeke, Erik H.W.G.M.
TITLE OF INVENTION: Cloning and expression of a new MCP receptor in glial cells
FILE REFERENCE: 2183-66420S
CURRENT APPLICATION NUMBER: US/10/623,472
CURRENT APPLICATION NUMBER: PC1/NL02/00039
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2001-01-18
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                              Sequence 15, Appl
Sequence 15, Appl
Sequence 153, Appl
Sequence 316, App
Sequence 756, Appl
Sequence 756, Appl
Sequence 756, Appl
Sequence 858, Appl
Sequence 887, Appl
Sequence 88, Appl
Sequence 88, Appl
Sequence 88, Appl
Sequence 308, Appl
Sequence 19, Appl
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Sequence 14, Appl
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Sequence 967, Sequence 3, Apl
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NAME/KKEY: misc. feature
LOCATION: (1) [1035)
OTHER INFORMATION: hCCR12 chemokine receptor sequence
5 US-10-029-386-22780

5 US-10-223-086-15

5 US-10-223-081-15

5 US-10-223-081-15

5 US-10-223-081-15

6 US-10-223-081-15

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8 US-10-305-654-15

9 US-10-305-654-15

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9 US-10-31-65-15

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1 US-10-305-120-3

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1 US-10-349-528-5

1 US-10-349-528-5

1 US-10-052-283-8

1 US-10-623-472-32

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Publication No. US20040096913A1
GENERAL INFORMATION:
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Best Local Similarity
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NewSULT 2 Westquence 11, action US/10039659 Publication	TO1.C. 37: linear MOLECULE TYPE: CDNA

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CURRENT APPLICATION NUMBER: US/10/754,071
CURRENT FILING DATE: 2004-01-07
PRIOR APPLICATION NUMBER: US 10/039,659
FRIOR FILING DATE: 2002-01-03
FRIOR FILING DATE: 1997-07-03
FRIOR FILING DATE: 1997-07-03
FRIOR FILING DATE: 1996-07-05
FRIOR FILING DATE: 1996-07-05
FRIOR FILING DATE: 1996-07-05
FRIOR FILING DATE: 1996-07-05
FRIOR APPLICATION NUMBER: US 60/028,329
FRIOR APPLICATION NUMBER: US 60/046,593
FRIOR FILING DATE: 1996-04
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn vergion 3.1
LENGTH: 1547
                                                                                                                                                                                                                                                                                  FEATURE:

NAME/KEY: CDS

LOCATION: (49)..(1116)

OTHER INFORMATION:
US-10-754-071-11
                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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   TGTGCATTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTCTGGAAGCATTTCTG
                                                                                  GCAGTTTCTAACTTGTGTTTCTTGCTTACCCTGCCCTTCTGGGCTCATGCTGGGGGGGTAT
                                                                                                                                              AATTGCCTTCTGACTGTGCAAAGGTACCTAGTGTTTTTGCACAAGGGCAACTTTTTCTCA
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                                                                  GCAGTITCIAACTIGIGITTTCITGCTIACCCTGCCCTTCTGGGCTCATGCTGGGGGGAT
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Publication No. US20040137578A1
GENERAL INFORMATION:
APPLICANT: Wang, Wei
APPLICANT: Gish, Kurt C.
APPLICANT: Schall, Thomas J.
APPLICANT: Schall, Thomas J.
APPLICANT: Schall, Thomas J.
APPLICANT: Schall, Thomas J.
APPLICANT: Schall, Albert
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Chemokine TECK Polypeptides
FILE REFERENCE: DX0589KIC US
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US-10-754-071-11
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GAGAGCGATGAGGCAGAGGATGTGAGTATGACGCCCAGGCATCTCAGCCCAGCTG
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; Sequence 12, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
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                                                                       TITGCCGTAATGGTAGTCTTCCTTCTGATGTGGGCGCCCTACAATATTGCATTTTTCCTG
                                                                                                                                          ACCCCACTTCAACCCAGGGGGCAGTCTGCACAAGGCACATCGAGGAAAAAAACCTGACCAT
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                   GTGCAAATGAGAAAACACTAAGGTTCAGGGAGCAGGGTATAGCCTTTTCAAGCTTGTT
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Sequence 11, Application US/10759860

Publication No. US20050074790A1

GENERAL INFORMATION:

APPLICANT: Gish, Kurt C.

APPLICANT: Gish, Kurt C.

APPLICANT: APLICANT: Alain P.

APPLICANT: Zlotnik, Albert

ITLE OF INVERTION: Methods for using chemokine TECK

FILE REFERENCE: DX0589XLD US

CURRENT APPLICATION NUMBER: US/10/759,860

CURRENT FILING DATE: 2004-01-16

PRIOR APPLICATION NUMBER: US 08/887,977

PRIOR FILING DATE: 1996-07-03

PRIOR PILING DATE: 1996-07-05

PRIOR APPLICATION NUMBER: US 60/028,329

PRIOR APPLICATION NUMBER: US 60/028,329

PRIOR PILING DATE: 1996-10-11

PRIOR PILING DATE: 1997-06-04

NUMBER OF SEG ID NOS: 26

SOFTWARE PLENCE IN VARIENT NET NOS: 26

SOFTWARE PLENCE NOS: 26
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Matches 1035, Conservative
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; OTHER INFORMATION:
US-10-759-860-11
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RESULT 6
US-10-741-600-13
Sequence 13, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: WYDEARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1776
                                                                                                             1102 GCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGTTTCCATCTGCGTAGTAAC 1161
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Pred. No. 0;
7; Mismatches
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Best Local Similarity 99.3%;
Matches 1028; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 12
LENGTHARE: ABSOCIATED CONTRACTOR OF THE CONTRACT
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larity 99.3%; Pred. No. 0;
Conservative 7; Mismatches
                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-10-741-600-12
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Best Local Similarity
Matches 1028; Conserv
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US-10-029-386-22780

US-10-029-386-22780

S. Sequence 22780 Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

ATILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR A
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Sequence 17557, Application US/10741600
Sublication No. US20050026169A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF CURRENT APPLICATION UNMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FasteSeQ for Windows Version 4.0
SEQ ID NO 17557
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             CTGGCCACTTTGCCTGAATWCRTGGTTTATAAACCTCAGATGGAAGACCAGAAATACAAG
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Best Local Similarity
Matches 1028; Conserv
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REPERENCE: P3235PLG10
CURRENT APPLICATION NUMBER: US/10/223,085
CURRENT APPLICATION NUMBER: US 10/081,056
PRIOR PELLOR DATE: 2002-08-16
PRIOR PELLOR DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/213,537
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR PELLOR DATE: 2000-07-20
PRIOR PELLOR DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR PELLOR DATE: 2000-07-25
PRIOR PELLOR DATE: 2000-07-25
PRIOR PELLOR DATE: 2000-07-25
PRIOR PELLOR DATE: 2000-07-25
PRIOR PELLOR DATE: 2000-08-27
PRIOR PELLOR DATE: 2000-08-27
PRIOR PELLOR NUMBER: US 60/222,695
PRIOR PELLOR DATE: 2000-08-27
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Publication No. US20030100497A1
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Georber, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Gudowski, Paul J.
APPLICANT: Hillan, Kenneth J.
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TT: Pan, James
TT: Stephan, Jean-Philippe F
TT: Watanabe, Colin K.
TT: Wood, William I.
TT: William I.
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OTHER INFORMATION: MAP TO U95626.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.99

OTHER INFORMATION: EXPRESSED IN BLAND, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN DUNG, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4

OTHER INFORMATION: EXT HUMAN HIT: BIB34559.1, EVALUE 0.00e+00

OTHER INFORMATION: MT HIT: G114736672, EVALUE 2.00e-63

US-10-029-386-22780
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TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AEOMICA.*.2 CURRENT APPLICATION NUMBER: US/10/029,386 CURRENT FILING DATE: 2001-12-20 NUMBER OF SEQ ID NOS: 34288 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 22780 LENGTH: 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.7%; Score 1031.8;
llarity 99.8%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 1033; Conserv
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APPLICANT: Weilladms, F.MICKEY
APPLICANT: Ye, Weilladms, F.MICKEY
APPLICANT: Ye, Weilladms, F.MICKEY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: CREATMENT OF DISORDERS INVOLVING ANGIOCENESIS
FILE REPERBNCE: P3235FLC3
CURRENT APPLICATION NUMBER: US/10/223,084
CURRENT PILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR FILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
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PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-08-27
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                                                                                                                                                                                                                                      Sequence 15, Application US/10223084
Publication No. US20030105011A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Geodward, Audrey
APPLICANT: Godward, Audrey
APPLICANT: Hillan, Kenneth J.
APPLICANT: Godwski, Paul J.
APPLICANT: Marsters, Scot A.
APPLICANT: Marsters, Scot A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
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0; Mismatches
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Best Local Similarity 99.8
Matches 1033; Conservative
                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                               US-10-223-085-15
SEQ ID NO 15
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; APPLICANT: Ferrara, Napoleone ; APPLICANT: Gerber, Hanspeter ; APPLICANT: Gerritsen, Mary E. ; APPLICANT: Goddard, Audrey ; APPLICANT: Godowski, Paul J. ; APPLICANT: Gurney, Austin L. ; APPLICANT: Marslers, Scot A.			FRIOR FILING DATE: 2000-00-23, PRIOR APPLICATION NUMBER: US 60/219,556; PRIOR FILING DATE: 2000-07-20; PRIOR FILING DATE: 2000-07-26; PRIOR FILING DATE: 2000-07-25; PRIOR FILING DATE: 2000-07-25; PRIOR FILING DATE: 2000-07-25; PRIOR FILING DATE: 2000-07-25		; PRIOK APPLICATION NUMBER: US 097643.057; PRIOR FILING DATE: 2000-08-17; PRIOR APPLICATION NUMBER: PCT/US00/23522; PRIOR FILING DATE: 2000-08-23 PRIOR FILING DATE: 2000-08-23		; LENGTH: 1475 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-223-088-15	Query Match 99.7%; Score 1031.8; DB 15; Length 1475; Best Local Similarity 99.8%; Pred. No. 0; Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps	Oy 1 ATGGCCAATTACACGCTGGCACCAGGATGAATATGATGTCCTCATAGAAGGTGAACTG 6	Oy 61 GAGAGCGATGAGCAGAGCAAGTATGACGCCCAGGCACTCTCAGCCCAGTG 1:		181 CTTATCCTGGTAAAATATAAAGGACTCAAACGCGTGGAAAATATCTATC	
99 GAGAGCGATGAGGCAATGTGACAAGTATGACGCCCAGGCACTCTCAGCCCAGCTG 148 121 GTGCCATCACTCTGCTGTGTTTGTGATCGGTGTCCTGGACAATCTCCTGGTTGTG 180 149 GTGCCATCACTCTGCTCTGCTGTTTTGTGATCGGTGTCCTGGACAATCTCCTGGTTGTG 208 181 CTTATCCTGGTAAAATATAAAGGACTCAAACGCGTGGAAAATATCTATC	GCAGTTTCTAACTTGTTTCTTGCTTACCCTGCCCTTCTGGGCTCATGCTGCTGGGGGGGG	CCCAIGNAAAATICTCATTGGACTGTACTTCGTGGGCCTGTACGGGGCATTTTTC AATTGCCTTCTGACTGCCAAAGGTACCTAGTGTTTTTGCACAAGGGCAACTTTTTCTCA AATTGCCTTCTGACTGCCAAAGGTACCTAGTGTTTTTTGCACAAGGGGAACTTTTTCTCA AATTGCCTTCTGACTGCCAAAGGTACCTAGTGTTTTTGCACAAGGGGAACTTTTTCTCA	CCGGGGGGGGGGCCCTGTGGGGTTTACAGGGGGGGGGGG	599 CIGGCATTTGCCIGAAACTCCTTCCTGCCAGCTGAAGAGCATTCTGGAAGCATTTCTG 600 541 TGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTCTGGAAGCATTTTCTG 600 569 TGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTCTGGAAGCATTTTCTG 628	601 ACTITAAAATGAACATTCGGTTCTTGTCCTCCCCTATTTATTTTACATTCTCTAT 660 	661 GTGCAAATGAGAAAAACACTAAGGTTCACGGAGCAGAGGGTATAGCCTTTTCAAGCTTGTT 720 	721 TTTGCCGTAATGGTAGTCTTCTGATGTGGGCGCCCTACAATATTGCATTTTCCTG 780 		AGTGTTCACATCACTAAACTCATCGCCACCCACCGCGCGCATCAACCCTCCCGGTAT	901 GCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGTTTCCATCTGCGTAGTAAC 960 	961 ACCCACTTCAACCCAGGGGCAGTCTGCACAAGGCACATCGAGGAAGAACCTGACCAT 1020 	1021 TCCACCGAAGTGTAA 1035 	
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269 GCAGTITCTAACITGTGTTTCTTGCTTACCCTGCCCTTCTGGGCTCATGCTGGGGGGGAT 328 301 CCCATGTGAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTACAGTGAGACATTTTTC 360 9 THACACGCTGGCACCAGAGGATGAATATGATGTCCTCATAGAAGGTGAACTG 88 TTACACGCTGGCACCAGAGGATGAATATGATGTCCTCATAGAAGGTGAACTG 0; Gaps 99.7%; Score 1031.8; DB 15; Length 1475; y 99.8%; Pred. No. 0; rvative 0; Mismatches 2; Indels 0; G iens a & ð

RESULT 11
US-10-223-088-15; Sequence 15, Application US/10223088; Publication No. US2030105012A1; GENERAL INFORMATION:

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329 CCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTACAGTGAGACATTTTC 388
FILE REPERENCE: P3235P1C2

CURRENT APPLICATION NUMBER: US/10/223,090

CURRENT PILING DATE: 2002-08-16

PRIOR FILING DATE: 2002-02-20

PRIOR PLING DATE: 2000-06-23

PRIOR PILING DATE: 2000-06-23

PRIOR PILING DATE: 2000-06-23

PRIOR PILING DATE: 2000-07-26

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US-10-223-090-15
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             CCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTACAGTGAGACATTTTTC 388
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APPLICANT: Baker, Kevin P.
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Geddard, Audrey
APPLICANT: Goddwaki, Paul J.
APPLICANT: Goddwaki, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hilan, Kenneth J.
APPLICANT: Hilan, Kenneth J.
APPLICANT: Hilan, Kenneth J.
APPLICANT: Pan, James Scot A.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: William P. Mickey
APPLICANT: William P. Mickey
APPLICANT: William COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
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; Publication No. US20030105013A1
; GENERAL INFORMATION:
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569 TGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTCTGGAAGCATTTTCTG 628
                                                                                      GTGCAAATGAGAAAAACACTAAAGGTTCAGGGAGCAGAGGTATAGCCTTTTCAAGCTTGTT 720
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APPLICANT: Gerrara, Napoleone
APPLICANT: Gerrara, Napoleone
APPLICANT: Gerrara, Napoleone
APPLICANT: Gerrara, Napoleone
APPLICANT: Goddwaki, Paul J.
APPLICANT: Goddwaki, Paul J.
APPLICANT: Goddwaki, Paul J.
APPLICANT: Goddwaki, Paul J.
APPLICANT: Gornerb, Austin L.
APPLICANT: Marsters, Scot A.
APPLICANT: Marsters, Con A.
APPLICANT: Maranabe, Colin K.
APPLICANT: Watlan James
APPLICANT: Watlan I.
APPLICANT: Wood, William I.
APPLICANT: William Date: 2000-06-23, OF PRIOR FILING DATE: 2000-06-23
FRIOR FILING DATE: 2000-07-26
FRIOR APPLICATION NUMBER: US 60/220, 664
FRIOR FILING DATE: 2000-07-25
FRIOR FILING DATE: 2000-07-25
FRIOR APPLICATION NUMBER: US 60/220, 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 15, Application US/10223087; Publication No. US20030109438A1
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APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
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PRIOR APPLICATION NUMBER 105 09/643,657

PRIOR PATING AND THE 2000 06-23

PRIOR PELING DATE: 2000 06-23

PRIOR APPLICATION NUMBER: PCT/US00/2328

PRIOR APPLICATION NUMBER: BCT/US00/2328

PRIOR PELING DATE: 2000 09-16

PRIOR PELING DATE: 2000 10-20

PRIOR PELING DATE: 2000 10-20

PRIOR PELING DATE: 2001 09-20

PRIOR PELING DATE: 2001 09-30

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APPLICANT: YE, Weilla B. F.MICKEY,
APPLICANT: YE, Weilla B. F.MICKEY,
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235PLC8
CURRENT APPLICATION NUMBER: US/10/23,083
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR PILING DATE: 2000-07-20
PRIOR PILING DATE: 2000-07-28
PRIOR PLING DATE: 2000-07-28
PRIOR PLING DATE: 2000-07-28
PRIOR PLING DATE: 2000-07-28
PRIOR PLING DATE: 2000-08-17
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llarity 99.8%; Pred. No. 0;
Conservative 0; Mismatches
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                                                                                                            RESULT 14
US-10-223-083-15
US-10-223-083-15
Sequence 15, Application US/1023083
Publication No. US20030119112A1
GENERAL INFORMATION:
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Stephan, Jean-Philippe
Watanabe, Colin K.
Wood, William I.
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APPLICANT: Gerrara, Napoleone
APPLICANT: Gerrara, Napoleone
APPLICANT: Gerriteen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
                       1049 TCCACCGAAGTGTAA 1063
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1021 TCCACCGAAGTGTAA
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Best Local Similarity
Matches 1033; Conserv
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LENGTH: 1475
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                       Score 1031.8;
Pred. No. 0;
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Query Match 99.7%; Score 1031.8; Best Local Similarity 99.8%; Pred. No. 0; Matches 1033; Conservative 0; Mismatches
             Hillan, Kenneth J
Marsters, Scot A.
Gurney, Austin L.
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ORGANISM: Homo sapiens
US-10-223-089-15
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                                                                            GCAGTITCTAACTIGIGITITCTIGCTIACCCIGCCCTTCTGGGCTCATGCTGGGGGGGAT
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120 180 148 240 360 AATTGCCTTCTGACTGCCAAAGGTACCTAGTGTTTTTGCACAAGGGCAACTTTTTCTCA 420 208 268 300 328 388 88 GCAGTITCTAACTIGIGITTCTTGCCTTACCCTGCCCTTCTGGGCCTCATGCTGGGGGCGAT ATGCCCAATTACACGCTGGCACCAGAGGATGAATATGATGTCCTCATAGAAGGTGAACTG GAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCCAGGCACTCTCAGCCCAGCTG GAGAGCGATGAGGCAGAGGAATGTGACAAGTATGACGCCCAGGCATCTCAGCCCAGCTG GIGCCATCACTCTGCTCTGCTGTGTTTTGTGATCGGTGTCCTGGACAATCTCCTGGTTGTG GTGCCATCACTCTGCTCTGCTGTTTTTGTGATCGGTGTCCTGGACAATCTCCCTGGTTGTG 1 ATGGCCAATTACACGCTGCCACAGAGGATGAATATGATGTCCTCATAGAAGGTGAACTG GCAGITICIAACTIGIGITITCTIGCTIACCCIGCCCTICIGGGCTCAIGCIGGGGGGGAI CCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTACAGTGAGACATTTTTC APPLICANT: Marsters, Scot A.
APPLICANT: Marsters, Scot A.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Recephan, Jean-Philippe F.
APPLICANT: Watanabe, Collin K.
APPLICANT: Watanabe, Collin K.
APPLICANT: William I.
APPLICANT: William I.
APPLICANT: Ye, Weilan
TITLE OF INVENTION: TREATMENT OF DISORBERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235PLC9
FILE REFERENCE: P3235PLC9
CURRENT APPLICATION NUMBER: US/10/223,089
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/213,556
PRIOR APPLICATION NUMBER: US 60/220,644
PRIOR APPLICATION NUMBER: US 60/220,644
PRIOR APPLICATION NUMBER: US 60/220,644
PRIOR PRILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,644
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Sequence 15, Application US/10223089;
Publication No. US20030125521A1;
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Gerber, Hangeter;
APPLICANT: Gerber, Hangeter;
APPLICANT: Gerriteen, Mary E.
APPLICANT: Goddard, Audrey;
APPLICANT: Goddard, Audrey;
APPLICANT: Goddwski, Paul J.

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Search completed: June 18, 2005, 15:44:32 Job time : 728.252 secs

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CO425383 UI-M-HU0-
BG8851388 602796680
BM247265 KO749D08-
CK839171 UI-R-AAI-
A1876375 UI-R-AAI-
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A1876375 UI-R-AAI-
CA578927 KO730H02-
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CA57993 KO732G02-
B1295780 UI-R-DK0-
CA579095 KO732G02-
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BK631033 BC631033
BE864135 UI-M-BHI-
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GenCore version 5.1.6
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773 7 CO959196 AA014646 mh17d07.r 288 1 AA034646 mh17d07.r 313 5 BX520969 BX520979 B	ALIGNMENTS 2111 bp mRNA linear HTC 03-APR-2004 thrary, clone:1810047105 product:chemokine (C-C) receptor G1:12841594	azoa; eria; d Haya y full	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kiteunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Sumi,N., Ishii,Y., Nakamuro,H., Sakkauchi,S., Ikegami,T., Kashikwaji,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B. Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Marsuura,S., Kawai,J., Okazaki,Y., Muramateu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. REXEN integrated sequence analysis (RISA) system384-format Genome Res. 10 (11), 1757-1771 (2000)
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FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

TITLE JOURNAL REFERENCE AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research

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Query Match
Best Local Similarity 99.94;
Matches 1082; Conservative
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

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Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki,Y.
Direct Submission
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Birck Submission
Submission Research Group, RIKEN Genoes Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@agsc.riken.jp,
RE:http://genome-gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGNGTCKVLVGLHSSGLYSBPSBNILLLAVQSYRVFSGQRLABSFTYSGCSLAB
AMATALSLPESVFYEPRMERQHKGERGFRPFLDIEAPLMKYVLTSKNIILLVALFPLL
VFIICCRQLRRRQSPRERQYDLHKPALVITGVFLLMMAPYNYVLTSRNIILVLAFPLL
KSSYHLDASVQVTQLVATTHCCVNPLLYLLDRKAFMRYLRSLFPRCNDIPYQSSGGY
QQAPPREGHRR PIELYSNLHQRQDII"
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CAVPAVGLLDNVLAVFILVKYKGLKNLGNIYPLNLALSNLCFLLPLPFWAHTAAHGES
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10 day old"
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1,-like 2 (MGD|MG1:1920904, GB|NM_017466,
BLASTN, 98*, match=2039)
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/db_xref="taxon:10090"

/clone="1810047105"
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Score 1081.4; DB 3
Pred. No. 4.9e-306;
0; Mismatches 1;
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Lowaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 558)

NIH-MGC http://mgc.nci.nih.gov/.
National Inatitutes of Health, Mammalian Gene Collection (MGC)

MIDUDIshed (1999)
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Email: cgapbs-rœmail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Inoryte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1286 row: d column: 03
High quality sequence state: 5
High quality sequence estop: 939.
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                                                                                     TTCACGACAGTGTCTTGTGGTGTATTGTTGCTGCGTGCATCCTGGCATGGCCATGGCTACTGCG
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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 885)
S 1 (bases 1 to 885)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CONTact: Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clond through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11056 row: a column: 22
High quality sequence stop: 828.
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1538 GAAGGTCATGGCAGGCCCATTGAACTGTACAATTTGCATCAAAGGCAGGATATAATA 1597
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885 bp mRNA linear EST 20-JUN-2001
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute (NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: GapDbareTemail.nih.gov
Tissue Procurement: Dr. Josef Lazar, Dr. Howard J. Jacob, Medical
College of Wisconsin
CONA Library Preparation: Open Biosystems
CONA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAMISTAS for consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                     CV116408 11339783 NIH MGC_270 Rattus norvegicus cDNA clone IMAGE:7445010 5', mRNA sequence.
                                                    766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 TCTTAGACGACTACCTGGACAACAGTGGGCCGGACCAAGTTCCGGCCCCCGAGTTCCTCT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 CCCCCCAGCAGGTGCTGCTGCTGCGGGGTGTTTGCGGTGGGTCTCTTGGACAACG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 TCATAGAGGATGACCTGGACAACAGTGGGACAGACCAGGCCCACCCCGAGTTCCTCT
                        GTACGACCTCCA - - CAAGCCGGCTCTTGTCATAACGGCCGTGTTCC - - TTTTGATGTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 713.
Location/Qualifiers
1. .770
                                                                                                                                                                                                   931 CGCCTTAACAACCCTGTGCCTTTTC 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Norway rat)
Rattus norvegicus
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EST.
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Matches 669; Conservative
                           111
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 ATGGATAACTACACAGTGGCCCCGGACGATGAATATGATGTCCTAATCTTAGACGACTAC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGACAACAGTGGGCCGGACCAAGTTCCGGCCCCCGAGTTCCTCTCCCCCCAGCAGGTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCAGTTCTGCTGCGGCGTGTTTGCGGTGGGTCTCTTGGACAACGTGCTGGCGGTGTTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCTTGGTGAAATACAAAGGACTCAAGAATCTGGGGAACATCTACTTCCTAAACCTGGCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTTCAAACCTGTGTTTCCTGCTTCCCCTGCCGTTCTGGGCCCATACTGCAGCACACGGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTCGGACTCCACTCCTCGGGCTTATAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCATGGCTACTGCGCTCTCTTTGCCCGAGTCTGTGTTTTATGAGCCTCGGATGGAAAGA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGAAACACACAAGTGTGCCTTTGGCAAACCTCACTTCTTGCCAATCGAAGCGCCGCTCTGG 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGAAA CACAAGTGTGCCTTTGGCAAACCTCACTTCTTGCCAATGGAAGGGCGCGCTCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 664.2; DB 4; Length 958;
Pred. No. 1.7e-183;
0; Mismatches 38; Indels 15
                                                 /organism="Mus musculus"
/mol_type="mRNA"
Location/Qualifiers
                                                                                                                  'strain="CZECH II"
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Best Local Similarity 93.4%;
Matches 752; Conservative
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                                                                                                                                                                       /clone_lib="NCI_CGAP_Maml"
//note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site_2: Not; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                            434
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                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                       8;
                                                                                                                                                                                                                                                                              Length 810;
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                                                                                                                                 samble"
                                                                                                                                                                                                                                                                           Score 585.8; DB 2;
Pred. No. 1.9e-160;
0; Mismatches 7;
                                        1. 810
/organism="Mus musculus"
/mol type="mxNA"
/strain="FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:3962910"
/tisuue_type="tumor, blopsy sam;/dev stage="3 months, virgin"
/lab_host="DH108"
      0
   Plate: LLAM9130 row: g column:
High quality sequence stop: 692.
Location/Qualifiers
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 97.8%;
Matches 658; Conservative
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Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 810)
Nat-Muc http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                  124 CGTTGGCAGTATTTATCTTGGCGAAATACAGAGGACTCAGGAATCCGGGGAACATCTACT
                                                                                                                                                                             CTGCCGCACATGGGGAAAGCCCGGGCAATGAGACTTGTAAAGTTCTTGTTGGACTCCACT
                                                                                                                                                                                                                 CCTCGGGCTTATACAGCGAGGTGTTTTCCAACATCCTCCTCCTTGTGCAAGGATACAGGG
                                                                                                                                                                                                                                        CCATGGGTTGTACAGGGAGACGCTTTGCAACATCCTCCTCCTTGTACAAGGATACAGGG
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                                             TGCTGGCGGTGTTTATCTTGGTGAAATACAAAGGACTCAAGAATCTGGGGAACATCTACT
                                                                                                                                                          CTGCAGCACACGGGAAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTCGGACTCCACT
                                                                                                                                                                                                                                                                           TGTTTTCCCAAGGGCGACTGGCCTCCATCTTCACGACAGTGTCTTGTGGTATTGTTGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can letter.//image.llnl.gov
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AUTHORS
TITLE
JOURNAL
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BE911886
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/clone_libe_worl_CGAP_Mam4"
//clone_libe_worl_CGAP_Mam4"
//note=morgan: mammary; vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Henniqhausen/Priscilla Purth,
and Difference for transgenic model: Li et al., Cell Growth
and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                                   420
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602796680F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4917762 5',
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                                              545
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 700)
                        486 CITICAAACTGTGTTTCCTGCTTCCCCTGCGTTTCTGGGCCCATACTGCAGACACGGG
                                                                                                                                                                                                   361 AGCGAGGTGTTTTCCAACATCCTCCTTGTGCAAGGATACAGGGTTTTCCCAAGGG
                                                                                                                                                                                                                                                                                                                                        666 CGACTCCCCCTCCTCACCACACAGTGTCTTGTGGTATTGTTGCGTGCATCCTGNCATGG
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10829 row: p column: 19
High quality sequence stop: 700.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NITH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/tissue_type="tumor, gross tissue"
/dev stage="5 months"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="NMRI"
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/lab_host="DH10B (T1 phage resistant)" |
/clone lib="NH1 BMAP HU0" |
/clone lib="NH1 BMAP HU0" |
/note="Organ: Eye; Vector: DXX-ABC; Site_1: ECOR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1* agarose
gel: First strand CDNA synthesis was primed with Oilgo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into DXX-ABC vector. The library tag
sequence located between the Not I site and the polyA tail
is AATATTAGC This library was created for the University
lows Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                                                                                             NIH 'MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 801)
        CO425383
UI-M-HUO-cra-i-17-0-UI.rl NIH BMAP_HUO Mus musculus cDNA clone IMAGE:30670960 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
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/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:10090"
/clone="IMAGE:30670960"
/tissue_type="whole eye"
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Mus musculus
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/done lib="NIA Mouse Hematopoietic Stem Cell
//lone lib="NIA Mouse Hematopoietic Stem Cell
(Lin-/C-Ktt-/Sca-1-) cDNA Library (Long)"
//note="vector: pSPORT! (Invitrogen); Site_1: SalI; Site_2:
NotI: Mouse CDNA project by the Laboratory of Genetics,
NotI: Mouse CDNA project by the Laboratory of Genetics,
Program, NIH (http://lgan.gr. mia.nih.gov/CDNA). This is
a long-transcript enriched CDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
obtained from Drs. Dennis Taub. Dan Longo (National Cancer Institute on Aaing, USA), Jonathan Keller (National Cancer Institute, USA). Double-stranded cDNAs were synthesized
with an Oilgo(dr) primer [Invitrogen: And Cancer Institute, USA). Double-stranded cDNAs were synthesized
by an Oilgo(dr) primer [Invitrogen: Jagated
to Lone-linker Lu-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range High fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The CDNAs were digested with Sal4-S. The
products were purified by phenol/chloroform and cloned into Sal1/NotI site of pSPORT! plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.1 kb. The library was constructed
by Yulan Piao (NIA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATCCCTATCAAAGTAGTGGAGGCTATCAGCAAGCGCCTCCAAGGGAAGGTCATGGCAG 1034
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llarity 100.0%; Pred. No. 8.2e-144;
Conservative 0; Mismatches 0; Indels
                           /organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6Ncr"
/db xref="nia8ST:KO749D08-3"
/db xref="taxon:10090"
/db xref="taxon:10090"
/tissue_type="Heam."
/tissue_type="Heam."
                                                                                                                                                                                                                  /dev stage="Age approx.10 weeks old"
/lab_host="DH108"
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Best Local Similarity
Matches 529; Conserv
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Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method
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                                                                                                                         13 CACAAGTGTGGCTTTGGCAAACCTCACTTCTTGCCAATCGAAGCGCCGCTCTGGAAGTAC
                                                                                                                                                                       GTTCTGACGTCAAAAAGATCATCTTGGTACTTGCTTTTCCTCTGCTGGTTTTTATAATC
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Contact: Dawood B. Dudekula
Contact: Dawood B. Dudekula
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Sulte 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0749 row: D column: 08
Seq primer: -21M13 Forward
High quality sequence stop: 540
POLYA*Yes.
                              ;
0
                                                                            CACAAGTGTGCCTTTGGCAAACCTCACTTCTTGCCAATCGAAGCGCCGC
                              Indels
       Pred. No. 1.2e-145;
0; Mismatches 1;
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99.88;
  Best Local Similarity 99.8
Matches 536; Conservative
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614 481 674 421 734

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RESULT 9 CK839171/c LOCUS

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

MEDLINE PUBMED COMMENT JOURNAL

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990 TAGTGGAGGCTATCAGCAAGCGCCTCCAAGGGAAGGTCATGGCAGGCCCATTGAACTGTA 1049
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood, K., Steptoe,M., Theiding,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Waterston,R., & Miller,R., & Shin,T., Jackson,Y., Cardenas,M., McCann,R., The WashU-NCI Mouse EST Project 1999
721 TGGTGGTATTGTTACGTGTGTCCTGGCATGGGCTGTGGCTGCCGCACTCTTTGCCCGA 662
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This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:991464
                                                                                                            661 AGCTGTGTTTTACGAGCCTCGGATGGAAAGACAGAAAACACAAAGTGCGGCTTTGGCAAACC
                                                                                                                                                                                                                                             244 GGCCTTTAGGAGCTATCTCTGCAGCCTGTTCCCACGGTGTAATGATCATCTCCCATTTCAAAG
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Washington University School of Medicine
Washington University School of Medicine
Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1810
Fax: 314 286 1810
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Mus musculus
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/clone="UI-R-AA1-zw-f-06-0-UI"
/dev stage="adult"
/dev stage="adult"
/lab host="DH10B (Life Technologies)"
/clone lib="UI-R-AAI"
/clone lib="UI-R-AAI"
/clone lib="UI-R-AAI"
/clone lib="UI-R-AAI"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AAI library is a normalized library constructed from 16.5 dpc rat atrium. The tag is a string of 5 nucleotides present between the Not I site and the oligo-dr track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996. Tissue provided by Jim Lin, Department of Biology, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Soares, MB
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
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cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
   61
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                                                                                                                                                                                                                                                                            UI-R-AA1-zw-f-06-0-UI.810 UI-R-AA1 Rattus norvegicus cDNA clone UI-R-AA1-zw-f-06-0-UI.3', mRNA sequence.
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----- 76; Indels
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches
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larity 87.4%; Pred. No. 2e-132;
Conservative 0; Mismatches 76;
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/strain="Sprague-Dawley"
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Rattus norvegicus
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rag_seq=gattc"
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Best Local Similarity
Matches 549; Conserva
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PEATURES

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CTGGACAACAGTGGGCCGGACCAAGTTCCGGCCCCCGAGTTCCTCTCCCCCCAGCAGGTG 120
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                            1 (bases 1 to 615)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                          National cancer

National Cancer

Unpublished (1997)

Other ESTS mash7filo.x1

Contact: Robert Strauberg, Ph.D.

Email: cgspbs-remail.nih.gov

This clone is available royalty-free through LLNL; contact the MAGE Consortium (info@image.llnl.gov) for further information. MGI:1459234

Seq primer: -40RP from Gibco

High quality sequence stop: 412.
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40.1%; Score 434; DB 2; L
Best Local Similarity 95.5%; Pred. No. 7.3e-116;
Matches 468; Conservative 0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                        1. .615
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGB:3822882"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="male"
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGTCCTAATCTTAGACGACTACCTGGACAACAGTGGGCCGGACCAAGTTCCGGCCCCC
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maa77f10.yl Soares mouse 3MbMS Mus museculus cDNA clone
IMAGE:3822882 5' similar to TR:035457 035457 PUTATIVE BETA
CHEMOKINE RECEPTOR. [1]; , mRNA sequence.
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          on wrong strand
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Pred. No. 7.8e-125;
0; Mismatches 6;
                                                                                                                                                /mol_type="mRNA"
/db_xref="texcon:10090"
/clone="imAdR:1974724"
/cell line="pituitary cell line"
/lab_hogt="SOLR"
Possible reversed clone: similarity
Seg primer: -40RP from Gibco
High quality sequence stop: 397.
Location/Qualifiers
                                                                                                                           organism="Mus musculus"
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BF662034.1 GI:11927168
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Best Local Similarity 98.7%;
Matches 468; Conservative
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554 bp mRNA linear EST 19-NOV-2002 CDN30H02-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-) IMAGE:30076501 5', mRNA sequence. CA578957
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(Lin-G-Kit-/Sca-1-) cDNA Library (Long)
/note="vector: pSPORTI (Invitrogen); Site_1: Sall; Site_2:
Not!, Mouse cDNA project by the Laboratory of Genetics.
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://Igsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAS were
obtained from Drs. Dennis Taub, pan Longo (National
Institute on Aging, USA), Jonathan Kaller (National
Institute, USA). Double-stranded cDNAs were synthesized
                                                                                   301 GAAAGCCTGGCAACGGAACTTGTAAAGTTCTTGTCGAACTCCACTCCTCGGGC-TTATA 359
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 554)
Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G., Alba,K., Taub,D., Longo,D.L., Keller,J. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
(Lin-/C-Kit-/Sca-1-) cDNA Library (Long)
Unpublished (2001)
Other ESTS KO730H02-3
                       472 GAAAGCCCTGGCAATGGGACCTGTAAAGTTCTTGTCGGACTCCACTCCTCGGGCNTTATA 531
CTTTCAAACCTGTGTTTCCTGCTTCCCCTGCCGTTCTGGGCCCCATACTGCAGCACACGGG 300
                                                                                                                                                                                                                532 CAGCGAGGTGTTTTCCAACATCCTCCTTGTGCAGGAATACAGGGGTGTTTTCNCAA 591
                                                                                                                                                                                                                                                          418 GGGCGACTGGCCTCCATCTTCACGACAGTGTTGTTGTTGCGTGCATCCTGGCA 477
                                                                                                                                                                                                                                                                                   360 CAGCGAGGTGTTTTCCAACATCCTCCTTCTTGTGCAAGGA--TACAGGGTGTTTTTCCCAA
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
and Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plater: K0730 row: H. column: 02
Seg primer: M13 Reverse
High quality sequence stop: 554
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db_xref="taxon:10090"
/db_xref="taxon:10090"
/dboxef="taxon:10090"
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(Lin-/C-KIt-/Sca-1-)"
(Lin-/C-KIt-/Sca-1-)"
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/strain="C57BL/6NCr"
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SM Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 721)

S NIH-MGC http://mgc.nci.nih.gov/.

S NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov

Tissue Procurement: Dr. Michael Brownstein Laboratory

CDNA Library Preparation: Michael Brownstein Laboratory

CDNA Library Preparation: Michael Brownstein Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 541.
                                                                                                                                                                      CBS98882 12785094 NIH MGC_178 MRNA linear EST 03-APR-2003
AGENCOURT_12785094 NIH MGC_178 Mus musculus cDNA clone
IMAGE:30295418 5', mRNA sequence.
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                                                                                                                                                                                                                                                               CB598882.1 GI:29516738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CTGGACAACAGTGGGCCGGACCAAGTTCCGGCCCCCGAGTTCCTCTCCCCCCAGCAGGTG
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                  Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
Small: capall prive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: capal@gau.grc.nia.nih.gov
Plate: K0749 row: D column: 08
Seq primer: M13 Reverse
High quality sequence stop: 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.5%; Score 406.6; DB 6; Length 552; 99.0%; Pred. No. 8e-108; tive 0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                            /tissue_type="Hematopoietic Stem Cell
(Lin-/c-Kit-/Sca-1-)"
(Adev atage="Age approx.10 weeks old"
/lab_hoste="DH108"
                                                                                                                                                                                                                                              /db_xref="nlaEST:K0749D08-5N"
/db_xref="taxon:10090"
/clone="NIA:K0749D08 IMAGE:30078283"
                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6NCr"
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                                                                                                                                                                Location/Qualifiers
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Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Alba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Hematopoietic Stem Cell
(Lin-/C-Kit-/Sca-1-) cDNA Library (Long)
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E. (bases 1 to 526)
Size at a constant of the constan
                                                                                                                                                                                                                                                                                                                                                                                                                                           K0732G02-5N NIA Mouse Hematopoletic Stem Cell (Lin-/c-Kit-/Sca-1-) CDNA Library (Long) Mus musculus CDNA clone NIA:K0732G02 IMAGE:30076681 5', mRNA sequence.
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GAAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTCGGACTCCACTCCTCGGGCTTATAC 360
                                          440 GAAAGCCCTGGCAATGGGACCTGTAAAGTTCTTGTCGGACTCCACTCCTCGGGCTTATAC
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The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.1 kb. The library was constructed by Yulan Piao (NIA)."
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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| APPLICANT: Wang, Wei
| APPLICANT: Gish, Kurt C. |
| APPLICANT: Schall, Thomas J. |
| APPLICANT: Schall, Thomas J. |
| APPLICANT: Schall, Thomas J. |
| APPLICANT: Vicari, Alain P. |
| APPLICANT: Zlotnik, Albert |
| TITLE OF INVENTION: Antibodies that bind chemokine TECK |
| TITLE OF INVENTION: ALLIBORIES |
| CURRENT FILING DATE: 1090-01-03 |
| PRIOR PPLICATION NUMBER: US 60/029, 977 |
| PRIOR PLILING DATE: 1996-07-05 |
| PRIOR APPLICATION NUMBER: US 60/028, 329 |
| PRIOR PLILING DATE: 1996-10-11 |
| PRIOR PLILING DATE: 1996-10-11 |
| PRIOR FILING DATE: 1997-06-04 |
| NUMBER OF SEQ ID NOS: 26 |
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; GENERAL INFORMATION:
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Best Local Similarity 65.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 398.4; DB 3;
Pred. No. 3.7e-117;
0; Mismatches 301;
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SCHECK, PALTICLA A.
REGISTRATION NUMBER: 33,777
REJECOMMUNICATION INPORMATION:
TELECHONE: 610-270-5031
TELEFAX: 610-270-5031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.5%;
Matches 662; Conservative
                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1050 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: 1
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                                                                                            544 CTGGCATGGGTAACAGCCATTCTGGCCACTTTGCCTGAATTCGTGGTTTATAAACCTCAG 603
                                                                                                                                                                                                                                                                            CTGGTTTTTATAATCTGCTGCAGGCAACTGAGGAGAAGGCAGAGGCTTCAGGGAGAGACAG 711
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 CTGGCATGGGCCATGGGCTACTGCGCTCTTTGCCCCGAGTCTGTGTTTTATGAGCCTCGG
                                                                                                                              ATGGAAAGACAGAAACACAAGTGTGCCTTTGGCAAACCTCACTTCTTGCCAATCGAAGCG
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| Sequence 1, Application US/08681192 |
| Patent No. 6287801 |
| Patent No. 6287801 |
| Patent No. 6287801 |
| APPLICANT: BERGSMA, DERK |
| APPLICANT: ELSHOURBAGY, NABIL |
| APPLICANT: SARAU, HENRY |
| TILLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNPDS78 |
| TILLE OF INVENTION: G-PROTEIN COUPLED SECRETOR HNPDS78 |
| NUMBER OF SEQUENCES |
| ADDRESSEE: SmithKline Beecham Corporation |
| STREET: 709 Swedeland Road |
| CITY: Ring of Pruseia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FABCESEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601,192
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ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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Sequence 2, Application US/08847296B

Patent No. 6271347

GENERAL INPORMATION:
APPLICANT: DAUGHERTY, BRUCE L.
APPLICANT: STCILIANO, JULIE A.
APPLICANT: STCILIANO, SALVATORE J.
APPLICANT: STRINGER, MARTIN J.
TITLE OF INVENTION: EOSINOPHIL EOTAXIN RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
Mismatches 372;
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 Conservative
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                   CTGGTTTTTATAATCTGCTGCAGGCAACTGAGGAAAAGGCAGAGCTTCAGGGAGAGACAG
                                                                                   TACGACCTCCACAAGCCGGCTCTTGTCATAACGGGCGTGTTCCTTTTGATGTGGGCGCCT
                                                                                                                                                 TACAACACTGTGCTTTTCCTGTCTGCTTTCCAGGAACACTTGTCCCTGCAGGATGAGAAG
                                                                                                                                                                                                               TGCGTCAACCCGCTGCTCTATTTGCTTCTTGACCGGAAGGCCTTTATGAGATACCTTCGC
                                              TITATITITACATITCTCTATGTGCAAATGAGAAAAACACTAAGGTTCAGGGAGCAGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/08771276;
Patent No. 6797811
GENERAL INFORMATION:
APPLICANT: Schweickart, Vicky L.
APPLICANT: Raport, Carol J.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                           1012 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAA 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,276
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                 952 AGCCTGTTCCCACGGTGCAATGATATCCCCTATCAA 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, STREET: 6300 Sears Tower, 233 S. Wacker Intr: Chicago STATE: 111inois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: No. 6797811and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33670
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 312-474 0448
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1059 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-711-276-19
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-08-771-276-19
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                                                                   104 TCTCCCCCCAGCAGGTGCTGCTGCTGCTGCGGCGTGTTTGCGGTGGGTCTCTTGGACA
                                                                                                                                                                                                       164 ACGTGCTGGCGGTGTTTATCTTGGTGAAATACAAAGGACTCAAGAATCTGGGGAACATCT
                                                                                                                                                                                                                                                                                                                                        224 ACTICCTAAACCIGGCACTICAAACCIGIGITICCIGCTICCCCIGCCGTICTGGGCCC
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Sequence 474, Application US/09826509

Sequence 474, Application US/09826509

Batent No. 6806054

GENERAL INFORMATION:

APPLICANT: Linw, Chen W.

APPLICANT: Linw, Chen W.

TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G

TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G

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TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G

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572 CAGTATATAGCTGGAGGCATTTCCACACTCTGAGAATGACCATCTTCTGTCTCGTTCTCC 631
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                                                                    CTCTGCTGGTTTTTATAATCTGCTGCAGGCAACTGAGGAGAAGGC-----AGAGCTTCA
                                                                                                                                     632 CTCTGCTCGTTATGGCCATCTGCTACACAGGAATCATCAAAACGCTGCTGAGGTGCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1068;
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ORGANISM: Homo sapiens
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US-'09-826-509-474
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US-09-826-509-474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 TGGCGGTGTTTATCTTGGTGAAATACAAAGGACTCAAGAATCTGGGGAACATCTACTTCC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 TANACCTGGCACTTCANACCTGTGTTTCCTGCTTCCCCTGCCGTTCTGGGCCCCATACTG 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 CCATTGTCCATGCTGTGTTTGCCCTTCGAGCCCGGACTGTCACTTTTGGTGTCATCACCA 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      587 AAGCGCCCCTCTGGAAGTACGTTCTGACGTCAAAATGATCATCTTGGTACTTGCTTTTC 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cr-----GAAGAGTTGTTTGAAGAGTCTTTTGCAGTGCTCTTTACCCAGAGGATA 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 183.2; DB 3; Length
Pred. No. 4.9e-48;
0; Mismatches 358; Indels
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MEDIUM TYPE: Disketter
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPRES: Passers of the compatible
COMBENTING SYSTEM: DOS
SOFTWARE: Passers of the compatible
COMBENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,296B
FILING DATE: 24-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/016,158
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 60/017,113
FILING DATE: 26-APR-1996
APPLICATION NUMBER: 60/017,113
FILING DATE: 26-APR-1996
ATTORNEY/AGENT UNMBER: 35,382
REGISTRATION NUMBER: 35,382
REGISTRATION NUMBER: 35,382
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3904
TELEFAX: 908-594-4720
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Best Local Similarity 54.3%;
Matches 446; Conservative 0
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LENGTH: 1065 Base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
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; MOLECULE TYPE: CDNA
US-08-847-296B-2
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APPLICANT: Gerard, No. 6537764ma P.
APPLICANT: Mackay, Charles R.
APPLICANT: Mackay, Charles R.
APPLICANT: Ponath, Paul D.
APPLICANT: Pont, Theodore W.
APPLICANT: Ofn, Shixin PROTEIN-COUPLED RECEPTOR GENE CCR3 AND TITLE OF INVENTION: ANTAGONISTS THEREOF
TITLE OF INVENTION: ANTAGONISTS THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
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US-08-720-565-3
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APPLICANT: Gerard, No. 6806061ma P.
APPLICANT: Mackay, Charles R.
APPLICANT: Ponath, Paul D.
APPLICANT: Post, Theodore W.
APPLICANT: Qin, Shixin
TITLE OF INVENTION: and Methods of Use Therefor
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Pred. No. 5.1e-48;
0; Mismatches 358; Indels
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CURRENT APPLICATION NUMBER: US/08/375,199B
CURRENT FILING DATE: 1995-01-19
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08375199B
Patent No. 6806061
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Best Local Similarity 54.3%;
Matches 446; Conservative
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ORGANISM: Homo sapiens
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; LOCATION: (37)
US-08-375-199B-3
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US-08-375-199B-3
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Batent No. 6500338

GENERAL INFORMATION:
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: LANGE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDR
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
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Pred. No. 5.3e-48;
0; Mismatches 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFENCE/FOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (660) 845-4166
INFORMATION FOR SEQ ID NO: 1085:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 54.3%;
Matches 446; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1201 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: PALO ALTO STATE: CALIFORNIA
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; CLONE: 91199579
US-09-016-434-1085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 TAMACCTGGCACTTTCAMACCTGTGTTTCCTGCTTCCCCTGCCGTTCTGGGCCCATACTG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---CAGCACACGGGGAAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTCGGACTCCACT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          432 ACACAGGCTTGTACAGCGAGATCTTTTCATAATCCTGCTGACAATGGACAGGTACCTGG 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 TGTTTTCCCAAGGGCGACTGGCCTCCATCTTCACGACAGTGTCTTGTGGTATTGTTGCGT 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCATCCTGGCATGGCCTACTGCGCTCTCTTTGCCCGAGTCTGTGTTTATGAGC 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CICGGATGGAAAGACAGAAACACAAGTGTGCCTTTGGCAAACCTTCACTTCTTGCCAATCG 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       587 AAGCGCCGCTCTGGAAGTACGTTCTGACGTCAAAATGATCATCTTGGTACTTGCTTTTC 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 CCCAGTTTGTGCCCCCCGCTGTACTCCCTGGTGTTCACTGTGGGCCTCTTGGGCAATGTGG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 regregregregrecrearaaaracaggaggerecgaarrargaccaacarcrecrec 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      312 TCAACCTGGCCATTTCGGACCTGCTCTTCCTCGTCACCCTTCCATTCTGGATCCACTATG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 TCAGGGGGCATAACTGGGTTTTTGGCCATGGCATGTGAAGCTCCTCTCAGGGTTTTATC 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 CCTCGGGCTTATACAGCGAGGTGTTTTCCAACATCCTCCTCCTTGTGCAAGGATACAGGG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       492 ccarrencearecrererrececerceaececesacrererriserereareaea 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCATCGTCACCTGGGCCTGGCAGCTGCTTCCTGAATTTATCTTCTATGAGA 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   663 cagrararagerigaaggearriceaeaerereagaargaeearerrerererereerieie 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
CLASSIFICATION 530
PROR APPLICATION DATA:
APPLICATION NUMBER: 19-JAN-1996
PRIOR APPLICATION NUMBER: 22,592
RILING DATE: 19-JAN-1995
ATFORNEY/AGENT INFORMATION:
NAME: BLOOK, DAVIG E:
REGISTRATION NUMBER: 22,592
RESERENCE/DOCKET NUMBER: 22,592
RESERENCE/DOCKET NUMBER: 22,592
TELEFRAK: 617-861-6340
TELEFRAK: 617-861-6340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1193 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: CDNA
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; LOCATION:
US-08-720-565-3
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SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERBWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING TANDER:
                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: pc-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-01
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 855-0555
TELEFAX: (650) 855-0555
INFORMATION FOR SEQ ID NO: 905: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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US-09-023-655-905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 CCTCGGGCTTATACAGCGAGGTGTTTTCCAACATCCTCCTCCTTGTGCAAGGATACAGGG 406
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                                                              Gaps
                                                           18;
Length 1201;
                                                           Indels
Query Match
16.9%; Score 183.2; DB 4;
Best Local Similarity 54.3%; Pred. No. 5.3e-48;
Matches 446; Conservative 0; Mismatches 358;
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Sequence 905, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: GLEftry J. Sealhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA

US-09-023-655-905

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                                                                                                         305 CCCAGTTTGTGCCCCCGCTGTACTCCCTGGTGTTCACTGTGGGCCTCTTGGGCAATGTGG
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| Patent No. 6265184
| GENERAL INFORMATION:
| APPLICANT: Gray et al.
| TITLE OF INVENTION: Chemokine Receptor Materials and Methods
| CORRESPONDENCE ADDRESS: 16
| CORRESPONDENCE Marchall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive
| STREET: 11linois | STATE: Illinois | STATE: I
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CTCTGCTGGTTTTTATAATCTGCTGCAGGCAACTGAGGAGAAGGC--
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APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 183.2; DB 4;
Pred. No. 6.6e-48;
0; Mismatches 358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cocke, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DET.
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PA-0001 US
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ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-01
TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 845-0555
TELEFAX: (650) 845-0466
INFORMATION FOR SEQ ID NO: 959:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 54.3%;
Matches 446; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
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CLONE: 91480480
US-09-023-655-959
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993 CTCTGCTCGTTATGGCCATCTGCTACACAGGAATCATCAAAACGCTGCTGAGGTGCCCCA 1052
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                                               GGGAGAGACAGTACGACCTCCACAAGCCGGCTCTTGTCATAACGGGCGTGTTCCTTTTGA 760
                                                                                                                                        761 IGIGGGCGCCTTACAACACTGTGCTTTTCCTGTCTGCTTTCCAGGAACACTTGTCCTGC 820
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                                                                                           1053 GTAAAAAAAAGGCGATGCGGCTCATTTTTGTCATCATGGCGGTGTTTTTCATTT
                                                                                                                                                                                                                                      18; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gray, Patrick W.
APPLICANT: Schweickart, Vicky L.
APPLICANT: Raport, Carol J.
TITLE OF INVENTION: Chemokine Receptor Materials and Methods
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "88-2B polynucleotide and amino acid
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6300 Sears Tower, 233 S. Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,276
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16.9%; Score 183.2; DB 4;
Best Local Similarity 54.3%; Pred. No. 7.1e-48;
Matches 446; Conservative 0; Mismatches 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: No. 6797811and, Greta E.
REGISTRATION NUMBER: 35,302
REFERNCE/DOCKET NUMBER: 27866/33670
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; OTHER INFORMATION: /= "88-2B ;
; OTHER INFORMATION: sequences"
US-08-771-276-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08771276
Patent No. 6797811
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1915 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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362..1426
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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LOCATION:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88-2B polynucleotide and amino acid
US-08-575-967A-3
                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
                                                                                                                                                                                                      ATCORNEY AGENT INFORMATION:
NAME: NO. 6265184and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-485-1900
TELEPHONE: 206-485-1900
TELEPHONE: 206-485-166
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 1915 base pairs
TYPE: nucleic acid
STRANBEDNESS: Single
    COMPUTER READABLE FORM:
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LOCATION: 362..1426
                                                                                                                                                                                       CLASSIFICATION: 435
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                                                                                                                                                              FILING DATE:
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COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOCTAMER: PETENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
CLASSIFICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
PRIOR APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REFERENCE/DOCKET NUMBER: LKS94-05A2
TELECOMMUNICATION NUMBER: LKS94-05A2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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US-08-720-565-1
                                                                        COUNTRY:
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APPLICANT: Butcher, Eugene C.
APPLICANT: Butcher, Eugene C.
APPLICANT: Butcher, Eric J.
APPLICANT: Butcher, Eric J.
APPLICANT: Runkel, Eric J.
APPLICANT: Pan, Junilang
ITILE Pan, Junilang
ITILE OF INVENTION: Method for Identifying Agents Which
ITILE OF INVENTION: Modulate Chemokine "MEC"-Induced Functions of CCR3 and/or
ITILE OF INVENTION: CR10
FILE REFERENCE: 1855.2010-003
CURRENT APPLICATION NUMBER: US, 09/638,914
FRIOR APPLICATION NUMBER: US. 09/638,914
FRIOR FILING DATE: 2000-08-15
FRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGACTGTGAGGGGACGAAGCATCTGGACCTGGTCATGCTGGTGACAGAGGTGATCGCCT 1051
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Pred. No. 7e-47;
0; Mismatches 360; Indels 18; Gaps
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NAME/KEY: CDS
LOCATION: (181)...(1248)
NAME/KEY: misc feature
LOCATION: (1291)...(1291)
OTHER INFORMATION: n = A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/09931381A Patent No. 6692922 GENERAL INFORMATION:
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Best Local Similarity 54.0%;
Matches 444; Conservative
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ORGANISM: Homo sapiens
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641 GCATCGTCACCTGGGGCCTGGCAGTGCTAGCAGCTCTTCCTGAATTTATCTTCTATGAGA
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Search completed: June 18, 2005, 12:14:51 Job time: 212.112 secs Sequence

Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 300, App Sequence 316, App Sequence 316, App Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 21, Appl Sequence 19, Appl Sequence 2, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli

Sequence 474, App Sequence 21, Appl Sequence 3, Appli

Sequence 63, Appl Sequence 1085, Ap Sequence 905, App

Sequence 100, App Sequence 959, App Sequence 5, Appli

Title: Perfect score:

Sequence:

nucleic

Run on:

Scoring table:

Minimum DB Maximum DB

Database

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Sequence 32, Application US/10623472

Sequence 32, Application US/10623472

Sequence 32, Application No. US20040096913A1

GENERAL INFORMATION:
APPLICANT: Bidex, Erik H.W.G.M.
APPLICANT: Biber, Knut
TITLE OF INVENTION: Cloning and expression of a new MCP receptor in glial cells
FILER REFERENCE: 2183-6042US
CURRENT APPLICATION NUMBER: US/10/623,472
CURRENT PILING DATE: 2003-07-18
PRIOR FILING DATE: 2002-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 18; Length 1083;
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LOCATION: (1).7(1083)
OTHER INFORMATION: mCCR12 chemokine receptor sequence
US-09-964-824A-100
US-10-641-643-959
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Pred. No. 0;
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Best Local Similarity
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ORGANISM: Mus sp.
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LENGTH: 1083
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                                                  Sequence 32, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 17557, A
Sequence 12780, A
Sequence 15, Appl
Sequence 15, Appl
                                                                                                                                                           June 18, 2005, 09:53:05; Search time 755.748 Seconds (without alignments) 8895.522 Million cell updates/sec
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1. /cgn2_6/ptodata/1/pubpna/PCT_NEW PUB.seq:*
2. /cgn2_6/ptodata/1/pubpna/PCT_NEW PUB.seq:*
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-741-600-12
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US-10-741-600-17557
US-10-022-386-22780
US-10-223-084-15
US-10-223-084-15
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Score

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RESULT 2
US-10-741-600-12
US-10-741-600-12

US-10-741-600-12

Bequence 12, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:

TITLE OF INVENTION: MICHEL et al.

TITLE OF INVENTION: MYCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WYCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT RILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: PSESEG FOR WINGOWS VERSION 4.0

SEQ ID NO 12

LENGTH: 1646
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Pred. No. 1.5e-131;
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Best Local Similarity 65.2
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US-10-741-600-17557

Sequence 17557, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OP DETECTION AND USES THEREOF

TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OP DETECTION AND USES THEREOF

TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 13, Application US/10741600
Sequence 13, Application US/10741600
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 13
LENGTH: 1776
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Sequence 22780
; Publication No. US20030194704A1
; GENERAL INFORMATION:
    APPLICANT: Penn, Sharron G.
    APPLICANT: Penn, Sharron G.
    APPLICANT: Hanzel, David K.
    TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
    FILE REFERENCE: AEOMICA-X-2
    CURRENT APPLICATION NUMBER: US/10/029,386
    CURRENT FILING DATE: 2001-12-20
    NUMBER OF SEQ ID NOS: 34288
    SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
    SEQ ID NO 22780
    LENGTH: 1140
                                                                                                                                                                                                                                                                                                                                                                               7888 ACATCGAGGGAAGCTGACCTTCCACCGAAGTGTAAACTAGCATCCACCAAATGCAA 7947
952 AGCCTGTTCCCACGGTGCAATGATATCCCCTATCAAAGTAGTGGAGGCTATCAGCAAGCG 1011
                                                                                                                     7828 cgcrerriccarcreceragiaacacececercaacecaagagacecageceacacaagac
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
OTHER INFORMATION: BY SIGNAL = 1.5
OTHER INFORMATION: BY SIGNAL = 1.4
OTHER INFORMATION: BY SIGNAL = 1.4
OTHER INFORMATION: NISSPROT HIT: 9114736572, EVALUE 0.000-60
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39.0%; Score 422; DB 16; Length 1140;
Best Local Similarity 65.5%; Pred. No. 3.1e-131;
Matches 709; Conservative 0; Mismatches 340; Indels 33
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86 CTGGAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCCAGGCACTCTCAGCCCAG 145
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS FULL REFERENCE: PRIZZSTENCE: PRIZZSTENCE: PRIZZSTENCE: PRIZZSTION NUMBER: US/01/023,085
CURRENT FILING DATE: 2002-08-16
PRIOR PLILING DATE: 2002-08-16
PRIOR PLILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR PLILING DATE: 2000-07-20
PRIOR PLILING DATE: 2000-07-20
PRIOR PLILING DATE: 2000-07-25
PRIOR PLILING DATE: 2000-07-26
PRIOR PLILING DATE: 2000-09-25
PRIOR PLILING DATE: 2000-09-25
PRIOR PLILING DATE: 2000-08-17
PRIOR PLILING DATE: 2000-08-23
PRIOR PLILING DATE: 2000-08-24
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Pred. No. 3.5e-131;
0; Mismatches 340; Indels 33
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Best Local Similarity 65.5%;
Matches 709; Conservative 0
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US-10-223-085-15
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Stephan, Jean-Philippe F.
Watanabe, Colin K.
Wood, William I.
Williams, P.Mickey
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Publication No. US20030100497A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
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APPLICANT: Berrara, Napoleone
APPLICANT: Gerrara, Napoleone
APPLICANT: Gerrara, Napoleone
APPLICANT: Gerrara, Napoleone
APPLICANT: Gerrara, Mary E.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Masters, Scot A.
APPLICANT: Masters, Colin K.
APPLICANT: William P. P.Mickey
APPLICANT: William P. P.Mickey
APPLICANT: Williams, D.Mickey
APPLICANT: Williams, D.Milliams, D.Mickey
APPLICANT: Williams, D.Milliams, D
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; Publication No. US20030105011A1
; GENERAL INFORMATION:
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                PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR PEPLOGATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR PELLING DATE: 2000-07-28
PRIOR PELLING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR PILING DATE: 2000-08-17
PRIOR PILING DATE: 2000-08-17
PRIOR PILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
REMAINING PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
REMAINING PRIOR APPLICATION NUMBER: PCT/US00/23328
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FILING DATE: 2000-07-25
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APPLICANT: GOGGGRAY, Pauli J.
APPLICANT: GOGGGRAY, Auguel J.
APPLICANT: Gurney, Auguin L.
APPLICANT: Mareters, Scot A.
APPLICANT: Mareters, Scot A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, P. Mickey
APPLICANT: Williams I.
APPLICANT: Williams, P. Mickey
APPLICANTON WUMBER: US 10/081,056
FRIOR PILING DATE: 2002-08-16
FRIOR APPLICATION NUMBER: US 60/219,556
FRIOR FILING DATE: 2000-06-23
FRIOR FILING DATE: 2000-07-26
FRIOR PILING DATE: 2000-07-26
FRIOR PILING DATE: 2000-07-25
FRIOR PILING DATE: 2000-07-26
FRIOR PILING DATE: 2000-07-26
FRIOR PILING DATE: 2000-07-26
FRIOR PILING DATE: 2000-08-02
FRIOR PILING DATE: 2000-08-03
FRIOR APPLICATION NUMBER: PCT/USON/23523
FRIOR APPLICATION NUMBER: PCT/USON/23523
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APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
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                                                                                                                                                                                                                                                                                                                                39.0%; Score 422; DB 15;
llarity 65.5%; Pred. No. 3.5e-131;
Conservative 0; Mismatches 340;
                                        - See
PRIOR FILING DATE: 2000-08-24
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 15
                                                                                                                                                 LENGTH: 1475
TYPE: DNA
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US-10-223-088-15
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 709; Conserv
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APPLICANT: Gerrara, Mapoleone
APPLICANT: Gerriten, Mary E.
APPLICANT: Gerriten, Mary E.
APPLICANT: Gerriten, Mary E.
APPLICANT: Gerriten, Martey
APPLICANT: Gerriten, Mattey
APPLICANT: Gerriten, Mattey
APPLICANT: Gerriten, Matter
APPLICANT: Gerriten, Matter
APPLICANT: Marsters, Scot A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Manosami I.
APPLICANT: Watanabe, Mailiams, P. Mickey
APPLICANT: Watanabe, Colin K.
APPLICANT: APPLICANT: Application data removed - See File Wrapper or PALM.
APPLICANT: Anne.
APPLICANT: 
TGCGTCAACCCGCTGCTCTATTTGCTTCTTGACCGGAAGGCCTTTATGAGATACCTTCGC
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Pred. No. 3.5e-131;
0; Mismatches 340; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, Application US/10223090 Publication No. US20030105013A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.0%;
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Best Local Similarity 65.5
Matches 709; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PILE REPREMENTATION NUMBER: US/10/223,087
CURRENT PELLING DATE: 2002-08-16
PRIOR PAPLICATION NUMBER: US 10/081,056
PRIOR PILLING DATE: 2002-02-20
PRIOR PILLING DATE: 2000-06-23
PRIOR PILLING DATE: 2000-06-23
PRIOR PILLING DATE: 2000-07-20
PRIOR PILLING DATE: 2000-07-20
PRIOR PILLING DATE: 2000-07-26
PRIOR PILLING DATE: 2000-07-28
PRIOR PILLING DATE: 2000-07-28
PRIOR PILLING DATE: 2000-07-28
PRIOR PILLING DATE: 2000-08-17
PRIOR PILLING DATE: 2000-08-27
PRIOR PILLING DATE: 2000-08-27
PRIOR PILLING DATE: 2000-09-16
PRIOR PILLING DATE: 2000-09-17
PRIOR PILLING DATE: 2000-09-18
PRIOR PILLING DATE: 2000-10-24
PRIOR PILLING DATE: 2000-10-24
PRIOR PILLING DATE: 2000-11-08
PRIOR PIL
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FILING DATE: 2000-12-20
PAPLICATION NUMBER: PCT/US00/34956
FILING DATE: 2000-12-20
APPLICATION NUMBER: US 09/767,609
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Stephan, Jean-Philippe F.
Watanabe, Colin K.
Wood, William I.
Williamg, P.Mickey
                                                                                                                                                                                                            Sequence 15, Application US/10223087
Publication No. UB20030109438A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                APPLICANT: Baker, Kevin P.
APPLICANT: Berrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary B.
APPLICANT: Goddard, Audrey
APPLICANT: Goddwaki, Paul J.
APPLICANT: Hillan, Kenneth J.
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PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/796,498
PRIOR PILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-03-01
PRIOR PILING DATE: 2001-03-01
PRIOR PILING DATE: 2001-03-01
PRIOR PILING DATE: 2001-03-04
PRIOR PILING DATE: 2001-03-04
PRIOR PILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-05-10
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-31
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Best Local Similarity 65.5
Matches 709; Conservative
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; ORGANISM: Homo sapiens
US-10-223-087-15
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      TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
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llarity 65.5%; Pred. No. 3.5e-131;
Conservative 0; Mismatches 340;
                                                                                                          PRIOR PELLING DATE: 2002-08-16
PRIOR PELLING DATE: 2002-02-0
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR PILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR PELLING DATE: 2000-07-26
PRIOR PELLING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,644
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR PILING DATE: 2000-07-25
PRIOR PELLING DATE: 2000-07-26
PRIOR PELLING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR PELLING DATE: 2000-08-17
PRIOR PELLING DATE: 2000-08-17
PRIOR PELLING DATE: 2000-08-24
PRIOR PELLING DATE: 2000-08-24
PRIOR PELLING DATE: 2000-08-24
                                  FILE REFERENCE: P3235P1C8
CURRENT APPLICATION NUMBER: US/10/223,083
CURRENT FILING DATE: 2002-08-16
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SEQ ID NO 15
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Best Local Similarity
Matches 709; Conserv
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US-10-223-083-15
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PRELICANT: Williams, P.Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Hillan, Kenneth J.
Marsters, Scot A.
Pan, James
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Wood, William I.
Williams, P.Mickey
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APPLICANT: Ferrara, Napoleo
APPLICANT: Gerber, Hanspete
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J
APPLICANT: Goddwski, Paul J
APPLICANT: Hillan, Kenneth
APPLICANT: Hillan, Kenneth
APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Ph
APPLICANT: Stephan, Jean-Ph
APPLICANT: Stephan, Jean-Ph
APPLICANT: Watanabe, Colin
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APPLICANT: Gerber, Hanspeleone
APPLICANT: Gerritsen, Mary E.
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddweki, Paul J.
APPLICANT: Hilan, Kenneth J.
APPLICANT: Hilan, Kenneth J.
APPLICANT: Harsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Marsters, Colin K.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Wood, William I.
APPLICANT: William P. P.Mickey
APPLICANT: William P. P.Mickey
APPLICANT: William B.
APPLICANT: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, Application US/10223089 Publication No. US20030125521A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Wary E.
APPLICANT: Goddard, Audrey
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Pred. No. 3.5e-131;
0; Mismatches 340; Indels
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR PILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-24
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        File
                                                                                                                                                                                                                                                                                                             Score 422; DB 16; 1 Pred. No. 3.5e-131; 0; Mismatches 340;
        - See
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 15
LENGTH: 1475
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 65.5%;
Matches 709; Conservative
                                                                                                                                                      TYPE: DNA
CRGANISM: Homo sapiens
US-10-223-081-15
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APPLICANT: Wood, William I.
APPLICANT: William S. P.Mickey
APPLICANT: William S. P.Mickey
APPLICANT: William S. P.Mickey
APPLICANT: William S. P.Mickey
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
TILLE REFERENCE: 2002-002-00
TITLE REFERENCE: 2002-002-00
CURRENT PILING DATE: 2002-002-00
FRIOR APPLICATION NUMBER: US 60/213,637
FRIOR PELING DATE: 2000-002-03
FRIOR PELING DATE: 2000-002-03
FRIOR FILING DATE: 2000-002-03
FRIOR FILING DATE: 2000-002-03
FRIOR PELING DATE: 2000-07-25
FRIOR FILING DATE: 2000-08-02
FRIOR PELING DATE: 2000-08-02
FRIOR PELING DATE: 2000-08-03
FRIOR PELING DATE: 2000-08-17
FRIOR PELING DATE: 2000-08-24
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Watanabe, Colin K.
Wood, William I.
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APPLICANT: Gerrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertleen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
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APPLICANT: BARET, KRVID F.

APPLICANT: Gerber, Hangeler

APPLICANT: Gerier, Hangeler

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Mary E.

APPLICANT: Goddard, Mary E.

APPLICANT: Goddard, Paul J.

APPLICANT: Materin L.

APPLICANT: Watherin L.

APPLICANTION NUMBER: US 60/220,664

PRIOR FILING DATE: 2000-07-25

PRIOR FILING DATE: 2000-00-07-25

PRIOR FILING DATE: 2000-00-07
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NUMBER OF SEQ ID NOS: 383
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/10223082
Publication No. US20030191059A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Baker, Kevin P.
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ORGANISM: Homo sapiens
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39.0%; Score 422; DB 17; Length 1475;
Best Local Similarity 65.5%; Pred. No. 3.5e-131;
Matches 709; Conservative 0; Mismatches 340; Indels 33
                                                       RESULT 15
US-10-305-654-15
IS-10-305-654-15

; Sequence 15, Application US/10305654
; Publication No. US20030224984A1
; GENERAL INFORMATION:
                                                                                                                                     APPLICANT: Baker, Kevin P.
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Searched:

Database

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1698)

Ansari-Lari,M.A., Liu,X.-M., Gorrell,J.H. and Gibbs,R.A.
Haplotype analysis of a gene cluster containing CCR5 and a new member of chemokine receptor gene family

L Unpublished

S Ansari-Lari,M.A., Liu,X.-M., Gorrell,J.H. and Gibbs,R.A.

Direct Submission

L Submitted (18-UUL-1997) Molecular and Human Genetics, Baylor

College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Location/Qualifiers

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IS Gish,K., McClanaban,T.K. and Woore,K.W.

Is Gish,K., McClanaban,T.K. and Woore,K.W.

L. Submitted (22-JUL-1997) Molecular Biology, DNAX Research Institute,

501 California Avenue, Palo Alto, CA 94304, USA

L. Coration/Qualifiers

1. 1790

/ Organism="Homo sapiens"

/ Mol Lype="mRNA"

/ Ab xrefe"taxon:9606"

/ Chromosome="3"

/ mapp="1921:3"

/ mapp="1921:3"

/ call type="primary monocytes; activated"

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CRAM: A Novel Human Chemokine Receptor-Like Gene Expressed
Activated Monocytes
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/gene="CRAM-B"
/prodon grart=1
/product="putative chemokine receptor"
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/db_xref="G1:3550070"
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Homo sapiens putative chemokine
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/protein id="AAH71682.1"
/db_xref="G1:47939092"
/db_xref="MIM:608379"
/db_xref="MIM:608379"
/translation="WANYTLABEDEYDVLIEGELESDEAEQCDKYDAQALSAQLVPSL CSAVFVIGYLDNLLVVXRGLKRYENTYLLNLANDANSNLCFLTLEPWAHAGGDPM CSANFVIGYLDNLLVVXRGLKRYENTYLHKGNFFSARRRVPCGIITSVLAWYTAI LATLEFEYVYRDOWEDGXKKCAFSRTPFLDMAPFLDTFWHISTLLAWNISTLDLAWYTAI LYVQWRKTLRFREQRYSLFKLVFAIMVVFLLMWAPYNIAFFLSTFKEHFSLSDCKSSY NLDKSVHITKLIATTHCCINPLLYAFLDGTFSKYLCRFFLLSTFKEHFSLSDCKSSY REEPDHSTEV"
                                              94305
                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 166 Row: i Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14043058. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGGGGGTAGAGCCACCAGGGGAATCAACAGTGGTTTCTCGTGCCCCTCAGGGTCAGGA 120
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DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 943 Meb site: http://www-shgc.stanford.edu Contact: (Dirkott, Mark) medepaxil.stanford.edu Dickson, Mar, Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:87900 IMAGE:5182006"
/tissue type="Brain, Lung, Testis, adult, pooled whole"
/clone lib="MIH MGC_115"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGCGGGTAGAGCCACCAGGGGAATCAACAGTGGTTTCTCGTGCCCCTCAGGGTCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGAGGCCTGGGGGAGCTTTTGACTTTTTTTTTTCAGTTGGTCCCTGAGCTCGGTGAGT
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/db_xrefe="LocusID:9034"
/db_xrefe="MIM:608379"
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99.8%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="Vector: pCMV-SPORT6"
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gene="CCRL2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="CCRL2"
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1 (basea 1 to 1755)

Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Stluer, C.D., Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Batr, N.K., Hopkins, R.F., Jordan, H., Morer, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Staplecon, M., Soares, M. B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Aramsec, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Aramson, R.D., Mullahy, S.J., Boardon, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Malzhy, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Yilalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffact, G.G., Blakeeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Wyers, R.M., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.
                                                                                                                                                                                                                                 1571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1632 TAAGATCACATAACTTAGGAAGTGGCAGAACTGATTCTCCCAGCCCTGGTAGCATTTGCTCA 1691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1692 GAGCCTACGCTTGGTCCAGAACATCAAACTCCTAAACCCTGGGGACAAACGACATGAAATA 1751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chemokine (C-C moif) receptor-like 2, mRNA (cDNA clone MGC:87900 IMAGE:5182006), complete cds.
BC071682
BC071682.1 GI:47939091
                                                      1452 AATCGGATACAGGAAGAAAAGGGAGGGGGGGCTGACTATTGCTAAGCACTGAATTTGTC
                                                                                                                                                       1441 TCAGGCACCGTGCAAGGCTCTTTACAAACGTGAGCTCCTTCGCCTCCTACCACTTGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1621 GAGCCTACGCTTGGTCCAGAACATCAAACTCCAAACCTGGGGACAAACGACATGAAATA
                                                                                                                                                                                                                             1512 rcaggcaccerecaegecrerrracaaacereaecrecreecerecraceaerrereea
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
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Homo sapiens
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9. 31. ENGLISHMENT AND ACCOUNT TO THE PROPERTY OF THE PROPERTY	1411 TCTTTACAAACGTGAGCTCCTTCGCCTCCTACCACTTGTCCATAGTGTGGATAGGACTAG 1500 1519 TCTCATTTCTCTGAGAAAACTAAGGCGGGAAATTTGTCTAAGATCACTTAACTAGG 1578 1501 TCTCATTTCTCTGAGAAAACTAAGGCGCGGAAATTTGTCTAAGATCACTTAGCTAGG 1578 1579 AAGTGGCAGAACTGATTCTCCAGCCTGGTAGCATTTGCTCAGAGCCTACGCTTGGTCCA 1638 11	BC025717 BC025717 Homo sapiens chemokine (C-C motif) receptor-like 2, mRNA (cDNA clone MGC:34104 IMAGE:5228561), complete cds. BC025717.1 GI:19343936 MGC. Homo sapiens (human) SM Homo sapiens (humanan) SM Homo sapiens (humanan known) SM H	Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villaion, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Shevchenko, Y., Fanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y. S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J. B., Jones, S.J. and Marra, M.A., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932 (Dasses I to 1770) Strausberg, R. Direct Submission Submitted (OG-WAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MCC help desk Email: Gapba-romail.nih.gov Contact: MCC help desk Email: Gapba-romail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, M. Benjamin.B., Mational Day National Institutes of Health Intramural Sequencing Center (NISC), Web site: http://www.nisc.nih.gov/ Contact: nisc.mgcAphalinh.gov Contac
143 TRICCTICATIONAMINIMA AND CONTRACTOR AND CONTRAC		RESULT 4 BC025717 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL PUBMED REFERENCE AUTHORS TITLE JOURNAL REMARK COMMENT
		TTGCCTTCTGACTGTGCAAAGGTACCTAGTGTTTTTGCACAAGGGCAACTTTTTCTCAGC TTGCCTTCTGACTGTGCAAAGGTACCTAGTGTTTTTTGCACAAGGGCAAATTTTTCTCAGC CAGAGGAGGAGGCGCCTGTGCTGTACAAGTGTCTTTTTTTT	TGCCATAATGGTAGTCTTCCTTCTGATGTGGGGCCCCTACAATATTGCATTTTTCCTGTC TGCCATAATGGTAGTCTTCCTTCTGATGTGGCGCCCCTACAATATTGCATTTTTCCTGTC CACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAGAGGCTACAATTTGCATTTTTCCTGTC CACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAGAGGCTACAATCTGGACAAAG TGTTCACATCACCTCACC

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McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 49 Row: o Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14043058.
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/note="grounyme: HCR, CRAM-B, CKRX,
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/db_xref="Mm:608379"
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                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0200690-A 15 03-JAN-2002;
Genentech, Inc. (US)
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CGACATGAAATAAATGTATTTTAAAACATC 1470
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX490908
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Homo sapiens
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i; Hominidae; Homo.
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 ATTITIACATTICICIATGIGCAAATGAGAAAACACIAAGGITCAGGGAGCAGAGGIAT
           ATTTTTACATTTCTCTATGTGCAAATGAGAAAAACCTTCAGGGAGCAGCAGGGAGT
                                         AATATTGCATTTTTCCTGTCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGC
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Antigenic peptides, such as for G protein-coupled receptors
(GPCRS), antibodies thereto, and systems for identifying such
antigenic peptides
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Mammalia; Eutheria; Primates; Catarrhini;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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85.7%; Score 1455.2; DB 6; Length 1645;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1457; Conservative 0; Mismatches 3; Indels 0;
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239 CCAGTGGGCAGTCTGAAGATGGCCAATTACACGCTGGCACCAGAGGATGAATATGATGTC 298
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Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
gene sets
Patent: WO 0194629-A 6461 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                 ATCAACCCTCTCCTGTATGCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGT
                                                          TTCCATCTGCGTAGTAACAÇCCCACTTCAACCCAGGGGGCAGTCTGCACAAGGCACATCG
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99.8%; Pred. No. 0;
:ive 0; Mismatches
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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TAAATGTATTTTAAAACATC 1644
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                                                                                                                                      DB 6; Length 1645
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WO 02061087-A 353 08-AUG-2002;
Biosciences, Inc. (US)
Location/Qualifiers
                                                                                                                                     Query Match 85.7%; Score 1455.2; Best Local Similarity 99.8%; Pred. No. 0; Matches 1457; Conservative 0; Mismatches
                                                         organism="Homo sapiens"
/mol_type="unassigned DNA"
/db xref="taxon:9606"
                                             1. .1645
Patent: WC
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KTLLRCRNEKKRHRAVRLIFTIMIVYFLFWAPYNIVLLLLMTFQEFFGLMNCSSSNRLD
QAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPER
ASSVYTRSTGEQEISVGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="Manytlapedeyuulegelesdeagcdkydaqalsaquvpsu
csayevigyldhijivyliivkykgikryeniyllinlavsnicfilitefwahdgddpm
ckiliglyfyglestefpkollifyqrylyfihkgnpfsarryvpcgiitsvlawytai
latlestyvykpqmedyrykleyfylpedetfwkhfiltwnisyllieiffp
lyvqyrkyllrrpqqxsgxslfklyfainvyfllwmapyniaffistfkehfslsdckssy
nldksvhitkliatthccinpllyafidgtfskylckfehrsuppreggsaggs
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YEGSGYFTAL QULRKSEBESHYARRARVWCAVGBGELKKVOWSGLSEGSVTGSSAST
TEDCIALVLKGEADANSLDGGYYTAGKCGLVPVLAENYKSQQSSDPDPNCVDRPVG
YLAVAVVRRSDTSLTWNSVKGKKGCHTAVDRTAGWNIPWGLLFNQTGSCKFDEYFSQ
CAPGSDPRSMICALCIGDEQGENKCVPNSNERYKYGYTGAFRCLAENAGDNAFVROVTV
LQNTDGNNNDAMARDLLCLDGKRKEVTEARSCHLAMAPWIHAVVSRUDKY
LKOVILLHQQAKFGRNGSDCPDKFCLFQSETKNILFNDNTECLARAAPWIHAVSRUDKVEP
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                                                                                                                                                                                                                                                                                                    /note="Identified as a gene by Grail Version 1.3c.
Translated sequence exhibits 42% sequence identity to CCR5
                                                                                                                                        /note="Putative mRNA identified by homology to CCR5 mRNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="DLSDEAERDEYELLCPDNTRKPVDKFKDCHLARVPSHAVVARSV/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="confirmed by similarity to lactoferrin protein,
encoded by GenBank Accession Number M73700, gi 186818"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96624 CCACAGGGCAGTCTGAAGATGGCCAATTACACGCTGGCACCAGAGGATGAATATGATGTC
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127884. .128068,130006. .130073,132023. .132164,
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737445. .137599,138436. .138610,139077. .>139255)
/product="lactoferrin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="confirmed by similarity to lactoferrin mRNA accession number M73700"
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99.8%; Pred. No. 0;
1ive 0; Mismatches 3; Indels 0; G
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/product="ccr6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAB57794.1"
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96642. .97676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="confirmed by similarity to Human monocyte chemoattractant protein 1 receptor (ccr2) alternatively spliced A-form, Encoded by GenBank Accession Number 108024, gi 1168965"
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chemoattractant protein 1 receptor (ccr2), Accession
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MRNA

Ses

gene

	RESULT 12 CQ714577 LOCUS DEFINITION Sequence 511 from Patent W002068579. ACCESSION CQ714577.1 GI:42275434 KEYWORDS SOURCE Homo sapiens CRANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof control of the	85.5%; Score 1452; DB 6; Length 1644; Similarity 99.7%; Pred. No. 0; 5; Conservative 0; Mismatches 5; Indels 0; Gaps CCAGTGGGCTGTGAAATTACAGGCTGGCACAGAGATATATGATGTCCACAGGGATCTGAAATTACAGGCTGGCACCAGAGGATGAATTATATCAGCTGGCACCAGAGATATATGATGTCCTACAGGGCAGTCTGAAAGATGACCAGAGGCAATTACAGCTGGCACCAGAGGATGAATATGATGTCCTCATAGAAGGTGAAATTACACGCTGGCAATGATGATGATGATGTCAGGGAAGGAA	Db 244 CTCATAGAAGGTGAACTGGAGGGGAGGCAATGTGACAAGTATGACGCCCAG 303 Qy 359 GCACTCTCAGCCCAGCTGCTCACTCTCTGCTGTTTTGTGATCGTGTCTCTG 418 Db 304 GCACTCTCAGCCCAGCTGGTGCTTACTCTGCTGTTTTGTGATCGTGTCTTG 363 Qy 419 GACATCTCCTGGTTGTGCTTATCCTGGTAAATATAAAGACTCCAAACGCTGGAAAT 478 Db 364 GACATCTCCTGGTTGTGCTTATCCTGGTAAATATAAAGACTCCAAACGCTGGAAAT 423 Qy 479 ATCTATCTTGTAGCTTTTCTAACTTGTTTCTTACTTGCTTACCCTGCCTTCTGG 538 Qy 479 ATCTATCTTCTAAACTTGGAGATTTCTAACTTGTTTCTTACCTTGCCTTCTGG 538 Qy 479 ATCTATCTTCTAAACTTGGAGAGTTTCTAACTTGTTTACCTTACCTTGCTTTCGG 538 Qy 539 GCTCATGCTGGAGAGTTTCTAACTTGTTTTCTTACCTTGCCTTCTGG 538
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Direct Submission
Unpublished
Upublished

(Labses 1 to 185437)

Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.

Direct Submission
Submission

Box 352145, Seattle, WA 98195, USA

(Labses 1 to 185437)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,

Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 18431)
2 (bases 1 to 18431)
2 (base, C., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                  ACO98613 185437 bp DNA linear PRI 01-AUG
Homo sapiens chromosome 3 clone RP11-24F11, complete sequence.
ACO98613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (01-AUG-2002) Genome Center, University of Washi
Box 352145, Seattle, WA 98195, USA
On Aug 1, 2002 this sequence version replaced gi:16445164.
Center: University of Washington Genome Center
Center Code: UWGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
Contact: uwgchtgs@u.washington.edu
Conter project Information
Conter project Information
Conter clone name: RF11.24F11 (bc0137)
Center clone name: RF11.24F11 (bc0137)
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET; 93% of reads
Chemistry: Dye-terminator Big Dye; 7% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 185398 bases at least Q30
Consensus quality: 185435 bases at least Q30
Consensus quality: 185435 bases at least Q20
Insert size: 185477; sum-of-contigs
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5': BAC-110P12 U95626, 111014-bp overlap
3': RP11-509121 (UMGC:bc0454) AC104304, 61294-bp
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1624 TAAATGTATTTTAAAACATC 1643
                                                                                                                                                                         AC098613.2 GI:22038607
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                                                                                                                                                                                                                                                                                                                                                      and Haugen, E.D.
                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                   DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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JOURNAL
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AUTHORS
TITLE
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Qy 1385 GGATACAGGAAGAAAAGGGAGAGGTGAGCTAACATTTGCTAAGCACTGAATTTGTCTCAG 1271 Db 1212 GGATACAGGAAGAAAAAGGGAGGGGGGGCTAACATTTGCTAAGCACTGAATTTGTCTCAG 1271 Qy 1445 GCACCGTGCAAGGCTTTACAAACGTCAGCTCCTTCGCCTCCTACCATGT 1504 1272 GCACCGTGCAAGGCTTTACAAACGTCAGCTCCTTCGCCTCTTGTCCATAGT 1331 Qy 1505 GTGGATAAGGACTAGTCTTTACAAAACTAAGGCCCCACTTGTCCATAGT 1331 Qy 1506 GTGGATAAGGACTAGTCTCTTTTCTTGAGAGAAAACTAAGGCCCGGAAATTTGTCTAAG 1564 Db 1332 GTGGATAAGTGTCTCATTTCTCTGAGAGAAAACTAAGGCCCGGAAATTTGTCTAAG 1564 Db 1392 ATCACTTAACTAGGAACTGATCTCCAGCCCTGGTAGCATTTGTCTCAGGC 1624 Db 1452 ATCACATAACTAGGAACTGATCTCCAGCCCTGGTAGCATTTGTCTCAGAGC 1624 Db 1452 CTACGCTTGGTCCAGAACTGATCCTCAACCCTGGGGGACAATTGCTCAGAGC 1684 Db 1452 CTACGCTTGGTCCAGAACTCCAAACCCTGGGGGACAACGAACATTAGAAAAATG 1684 Db 1452 CTACGCTTGGTCCAGAACTCCAAACCCTGGGGGACAAACGAACATGAAATAAAT	RESULT 15 AR526903 LOCUS LOCUS DEFINITION Sequence 11 from patent US 6723520. ACCESSION AR526903 VERSION AR526903.1 GI:53913793 KEYWORDS UNKNOWN. ORGANISM UNknown. ORGANISM Unknown. ORGANISM Unknown. TITLE Antibodies that bind chemokine teck JOURNAL Patent: US 6723520-A 11 20-APR-2004; FEATURES SOURCE JOURNAL Patent: US 6723520-A 11 20-APR-2004; FEATURES SOURCE //organism="unknown" //mol_type="genomic DNA"	Query Match 85.3%; Score 1448.2; DB 6; Length 1547; Best Local Similarity 99.8%; Pred. No. 0; 3; Indels 0; 6aps 0; Amtches 1450; Conservative 0; Mismatches 3; Indels 0; 6aps 0; Qy 245 GGCAGTCTGAAGATGGCCAATTACAGGCTGGCACCAGAGGATGAATATGATGTCCTCATA 132 Db 73 GGCAGTCTGAAGATGGCCAATTACAGGCTGGCAATGTGAACATTAGACGCCCAGGCACTCTCATA 132 AgaAGGTGAACTGGAGAGCGATGAGCAATGTGAACATGTGACCCCAGGCACTCTCTCATA 132 AgaAGGTGAACTGGAGAGCGATGAGCAATTGTGAATGACGCCCAGGCACTCTCTCATA 142 Db 133 GAAGGTGAACTGGAGCGATCACTCTGCTTGTTGTTGTTGTGTTCTGGTTCTGGTCTCTGGACAAT 152 Qy 365 TCAGCCCAGCTGGTGCATATCCTGGTGTTTGTGTTTGTGTTCTGGTGAAAATTCTAT 184 Db 193 TCAGCCAGTTGTGCTTATCCTGGTAAAATATAAAGGACTCAAACGCGTGGAAAATTCTAT 152 Qy 485 CTTCTAAACTTGGCAGTTTCTAACTTGTGTTTCTTGCTTACCTGGGCGTGTAT 16 Qy 545 GCTGGGGGGCGATCCCATTGTGTTTCTTGCTTACCTGGGGCTGTATACTGGGGCTGTACAGGGCTGT
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AF014958 1698 1 AGACGCTTCAGAGATCCTCT......TAAATGTATTTTAAAACATC 1698 Title: Perfect score:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Adpl3564 Renal cel	Ada38350 Human SNP	Ablee079 Human PRO	Abl95568 Human ang	Add10304 Human sec	Add11264 Human sec	Add37057 Human sec	Ade41265 Human sec	Adh43448 Human PRO	Adk82793 Human PRO	Abz42782 Human che	Adn95729 Human BEC	Adp24442 PRO polyp	Ads75309 Human CCR	Abd20648 Human pul	Abd20815 Human pul	Aaa34983 Human ade	Aaa35150 Human ade	Aaf21272 Human low	Human
SOUTHWATES	ΩI	ADP13564	ADQ38350	ABL88079	ABL95568	ADD10304	ADD11264	ADD37057	ADE41265	ADH43448	ADK82793	ABZ42782	ADN95729	ADP24442	ADS75309	ABD20648	ABD20815	AAA34983	AAA35150	AAF21272	AAF21105
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	Query	0.001	7.6	9.9	9.5	6.5	6.5	6.5	6.5	6.5	9.5	5.7	5.7	5.7	85.7	5.7	5.7	5.7	5.7	5.7	5.7
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6 ABL68124 6 ABT11034 10 ABZ36966 10 ABZ36799 3 AAA35151 1 ABD20816	10 ARX26967 13 ADQ38349 2 AAV35419 10 ABX35537 12 ADG67844 10 ACA56158 12 ADI55954	11 ADP03560 11 ADP03560 12 ACH89585 12 ADS32092 6 ABS32092 6 ABS32092 2 AAV04641 6 AAS17436 6 AAD132884
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1455.2 1455.2 1455.2 1455.2 1455.2 1455.2		1267.6 1161.4 1033.4 1033.4 1031.8 981.2 981.2 591.2 597.8
22 23 24 25 26 26 27	888888888888888888888888888888888888	0 333333333333333333333333333333333333

ALIGNMENTS

ds; diagnosis; non-blood disease; solid tumor; gene expression; peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer; head/neck cancer; differential expression. Renal cell carcinoma differentially expressed gene #300. ADP13564 standard; DNA; 1698 BP. 21-NOV-2003; 2003WO-US037481. 21-NOV-2002; 2002US-0427982P. 03-APR-2003; 2003US-0459782P. 26-AUG-2004 (first entry) (AMHP) WYETH.

(WINN) THINB N C.

(TREP/) BURCZYNSKI M E.

(TREP/) TREPICCHIO W L.

(STOWN) DORNER A.

(STOWN) STOWER J A.

(SLON/) SLONI D K. WO2004048933-A2. Homo sapiens. 10-JUN-2004. ADP13564; RESULT 1 ADP13564 SX H L L X X B B B B B B B X B X B X B X X B X X X X X X X X X B X

Diagnosing non-blood disease such as solid tumor, involves comparing differential expression profile of specific genes in peripheral blood sample of subject with reference expression profile of specific genes. WPI; 2004-460799/43. Twine NC, Sloni DK;

Stover JA;

Dorner A,

Trepicchio WL,

Burczynski ME,

Disclosure; SEQ ID NO 300; 350pp; English.

N

The invention relate to a method of diagnosing (MI) non-blood disease such as solid tumor by providing peripheral blood sample of human having con-blood disease, and comparing an expression profile of specific genes in the peripheral blood sample to reference expression profile of the genes, where each of the genes is differentially expressed in peripheral blood monounclear cells (PBMCs) of patients having the disease as compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from con-blood disease such as solid tumor. The solid tumor is chosen from arcinoma (RCC), prostate cancer and head/neck ancer. The peripheral blood sample (claimed). (MI) is useful for identifying sample is a whole blood sample (claimed). (MI) is useful for identifying genes that are differentially expressed in peripheral blood samples is solated at different solid tumors. This sequence corresponds to a gene that is sland or other solid tumors. This sequence corresponds to a gene that is differentially expressed and detected by the method of the invention. (Note: this sequence is not given as part of the printed specification but was obtained from MIPO in electronic format at

Sequence 1698 BP; 434 A; 413 C; 392 G; 459 T; 0 U; 0 Other;

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1080 1320 1500 1560 1080 1200 1380 1621 GAGCCTACGCTTGGTCCAGAACATCAAACTCCAAACCCTGGGGACAAACGACATGAAATA 1680 1201 CCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACAAGGCACATCGAG 1260 840 900 960 TAGTGTGGATAGGACTAGTCTCTTTCTCTGAGAAGAAACTAAGGCGCGGAAATTTGTC TTTTACATTTCTCTATGTGCAAATGAGAAAAACACTAAGGTTCAGGGAGCAGAGGTATAG CTGGAAGCATTTTCTGACTTTAAAAATGAACATTTCGGTTCTTGTCCTCCCCCTATTTAT CTGGAAGCATTTTCTGACTTTAAAAATGAACATTTCGGTTCTTGTCCTCCCCCTATTAT TTTTACATTTCTCTATGTGCAAATGAGAAAACACTAAGGTTCAGGGAGCAGAGGTATAG TATTGCATTTTTCCTGTCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAG TATTGCATTTTTCCTGTCCACTTTCAAAGAACACTTCTCCCCTGAGTGACTGCAAGAGGAG GGAAGAACCTGACCATTCCACCGAAGTGTAAACTAGCATCCACCAAATGCAAGAAGAATA AACATGGATTTTCATCTTTCTGCATTATTTCATGTAAATTTTTCTACACATTTGTATACAA TAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAAACTAAGGGCGCGGAAATTTGTC TAAGATCACTTAACTAGGAAGTGGCAGAACTGATTCTCCCAGCCCTGGTAGCATTTGCTCA GAGCCTACGCTTGGTCCAGAACATCAAACTCCAAACCCTGGGGACAAACGACATGAAATA CCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACAAGGCACATCGAG GGAAGAACCTGACCATTCCACCGAAGTGTAAACTAGCATCCACCAAATGCAAGAATA AACATGGATTTTCATCTTTCTTGCATTATTTCATGTAAATTTTCTACACATTTGTATACAA AATCGGATACAGGAAGAAAAGGGAGAGGTGAGCTAACATTTGCTAAGCACTGAATTTGTC TCAGGCACCGTGCAAGGCTCTTTACAAACGTGAGCTCCTTCGCCTCCTACCACTTGTCCA TAAGATCACTTAACTAGGAAGTGGCAGAACTGATTCTCCAGCCCTGGTAGCATTTGCTCA AATGTATTTAAAACATC 1698 AATGTATTTTAAAACATC 1021 1081 1081 1261 1381 1381 1441 1501 1501 1561 1691 721 781 841 901 1021 1201 1261 1321 1321 1441 1561 1621 1681 781 841 901 961 961 721 유 ò 셤 ò g ò 엄 8 요 ò 셤 ò a à 셤 ò g ò 요 ò g ð g à 셤 ઠે g ઠે 임 ઠે g ò 셤 Š

RESULT 2 ADQ38350 ID ADQ36

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GGGCAACTTTTTCTCAGCCAGGAGGAGGTGCCCTGTGGCATCATTACAAGTGTCCTGGC

BP. ADQ38350 standard; DNA; 1776 g ò 셤 ò 셤 ò

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ADQ38350;
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Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids. Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human; gene; ds. Human SNP containing myocardial infarction-associated gene, SEQ ID 13. Iakoubova O; 20-DEC-2002; 2002US-0434778P. 10-MAR-2003; 2003US-0453135P. 30-APR-2003; 2003US-0466412P. 23-SEP-2003; 2003US-0504955P. 22-DEC-2003; 2003WO-US040978 (first entry) Devlin JJ, (APPL-) APPLERA CORP WPI; 2004-533949/51. P-PSDB; ADO39178 WO2004058052-A2 Homo sapiens. 18-NOV-2004 15-JUL-2004 Cargill M,

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Claim 7; SEQ ID NO 13; 145pp; English.

The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual, so nucleic acids, where the presence of the SNP is correlated with an or altered risk for myocardial infarction in the individual. The invention further comprises an isolated nucleic acid molecule comprising at least currenter comprises; an isolated nucleic acid molecule comprising at least B contiguous nucleotides where one of the nucleotides is an SNP given in the specification; an isolated polypeptide caid sequence given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an inthe specification; an integen-binding of ragment; an amplified polymucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in capacitication and which is between about 16 and 1000 nucleotides in contributed by a kit for detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and control of contenting an applituance of the invention may be used in gene therapy. The composition for treating of the invention may be used in gene therapy. The composition for treating or preventing myocardial infarction. This composition for treating or preventing myocardial infarction. This composition for treating or preventing myocardial infarction. This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the MIPO website.

Sequence 1776 BP; 456 A; 425 C; 412 G; 472 T; 0 U; 11 Other;

DB 13;

1 AGACGCTTCAGAGATCCTCTGGAGGCCTGGGGGAGCTTTTGAGTACTTTATTTCAGTTGG Gaps ö 0; Indels 99.7%; Score 1693.6; 99.4%; Pred. No. 0; ive 11; Mismatches Best Local Similarity ya. ** Matches 1687; Conservative 72

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1031 1211 180 240 300 360 420 480 540 9 9 191 251 CATAGAAGGTGAACTGGAGAGCGATGAGGCAGAGGAATGTGACGAGTATGACGCCCAGGC 431 491 551 611 671 731 720 791 780 840 900 960 CCCACAGCTCCCGGATGCTGGGTCTGGAGGCTGCGCCCTTCSCCTGCAGGAGCTCAGCCC 311 851 911 971 TCCCTGAGCTCGGTGAGTGGGGCGGGTAGAGCCACCAGGGGAATCAACAGTGGTTTCTCG 132 TCCTGAGCTCGGTGAGTGGGCGGGTAGAGCCACCAGGGGAATCAACAGTGGTTTCTCG rececteaggereaggeagrergareaaaggagggearecaergreegggeearr CATAGAAGGTGAACTGGAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCCAGGC ACTICTCAGCCCAGCTGCCATCACTCTGCTCTGCTGTTTGTGATCGGTGTCCTGGA CAATCTCCTGGTTGTGCTTATCCTGGTAAAATATAAAGGACTCAAACGCGTGGAAAAATAT TCATGCTGRKGGCGATCCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTA CAGTGAGACATTTTTCAATTGCCTTCTGACTGTGCAAAGGTACCTAGTGTTTTTGCACAA 852 AGACCAGABAATACAAGTGTGTGTATTAGCAGAACTCCCCTTCCTGCCAGCAGATGAGACATT TTTTACATTTCTCTATGTGCAAATGAGAAAAACACTAAGGTTCAGGGAGCAGAGGTATAG 972 TTTTACATTTCTCTATGTGCAAATGAGAAAAACACTAAGGTTCAGGGGGGCAGCAGTATAG CCCACAGCTCCCGGATGCTGGGTCTGGGCTGCGCCCTTCCCCTGCAGGAGCTCAGCCC AGTGGGCAGTCTGAAGATGGCCAATTACACGCTGGCACCAGAGGATGAATATGATGTCCT CAATCTCCTGGTTGTGCTTATCCTGGTAAAATATAAAGGACTCAAACGCGTGGAAAATAT TCATGCTGGGGGGGATCCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTA CAGTGAGACATTTTTCAATTGCCTTCTGACTGTGCAAAGGTACCTAGTGTTTTTGCACAA 732 GGGMAACTTTTCTCAGCCAGGAGGAGGGTGCCCTGTGGCATCATTACAAGTGTCCTGGC ATGGGTAACAGCCATTCTGGCCACTTTGCCTGAATACGTGGTTTATAAACCTCAGATGGA AGACCAGAAATACAAGTGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATT CTGGAAGCATTTTCTGACTTTAAAAATGAACATTTCGGTTCTTGTCCTCCCCCTATTAT cregaagcarrrrcaacrrraaaaardaacarrrcegrrcrrerccccccrarrrar 032 CCTTTTCAAGCTTGTTTTTGCCRTAATGGTAGTAGTTCTTCCTTCTGATGTGGGCGCCCTACAA 1021 TATTGCATTTTTCCTGTCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAG CTACAATCTGGACAAAAGTGTTCACATCACTAAACTCATCGCCACCCCCCCGCTGCAT CTACAATCTGGACAAAAGTGTTCACATCACTAAAACTCATCGCCACCACCACCACTGCTGCAT **GGGCAACTTTTTCTCAGGCGAGGAGGGTGCCCTGTGGCATCATTACAAGTGTCCTGGC** rarrecarrirrecreterecarrireaagaacaerrecereagicaerecaagaecae 312 372 361 432 612 61 192 252 672 121 181 241 301 421 492 481 552 541 601 781 912 901 1092 1081 1152 661 721 841 961

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                                                                                                                                                                                                                                                                                   1691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; theumatoid arthritis; myocardial infarction; thromopophiebitis; tymoual angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
                                                                                                                                                                                                  TCAGGCACCGTGCAAGGCTCTTTACAAACGTGAGCTCCTTCGCCTCCTACCACTTGTCCA
         CAACCCTCTCCTGTATGCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGTTT
                                   CCATCTGCGTAGTAACACCCCCACTTCAACCCAGGGGGCAGTCTGCACAAGGCACATCGAG
                                                    ccarcrectagradacacccacricaacccageeecagrerecacaaeecarcaae
                                                                                          1332 GGAAGAACCTGACCATTCCACCGAAGTGTAAACTAGCATCCACCAAATGCAAGAAGAATA
                                                                                                                                AACATGGATTTTCATCTTTCTGCATTATTTTCATGTAAATTTTCTACACATTTTGTATACAA
                                                                                                                                                   AATCGGATACAGGAAGAAAGGGAGAGGTGAGCTAACATTTGCTAAGCACTGAATTTGTC
                                                                                                                                                                                        TCAGGCACCGTGCAAGGCTCTTTACAAACGTGAGCTCCTTCGCCTCCTACCACTTGTCCA
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                                                                                                             AACATGGATTTTCATCTTTCTGCATTATTTCATGTAAATTTTCTACACATTTGTATACAA
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2000US-0219556P.
2000US-0220624P.
2000US-0220664P.
2000WO-US020710.
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25-JUL-2000;
25-JUL-2000;
28-JUL-2000;
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ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rhemmatoid arthritis, angina, myocardial infarctions, thromophlebitis, lymphangitis, tumour anging, may beast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL8826, represent primers and probes used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGAGCTCAGCCCAGTGGGCAGTCTGAAGATGGCCAATTACACGCTGGCACCAGAGGATGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAGCTCAGCCCAGTGGGCAGTCTGAAGATGGCCAATTACACGCTGGCACCAGAGGATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      One hundred and eighty seven nucleic acids encoding PRO polypeptides useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
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Hillan KJ, Marsters SA, Pan J,
Williams PM, Wood WI, Ye W;
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Pred. No. 0;
0; Mismatches
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2001US-00767609.
2001US-00796498.
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2001US-00802706.
2001US-00808689.
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2001US-00828366.
2001US-00854208.
2001US-00854280.
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2000WO-US030952
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Stephan JF, Watanabe CK,
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Matches 1469; Conservative
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                                             24-AUG-2000;
07-SEP-2000;
18-SEP-2000;
14-SEP-2000;
24-OCT-2000;
08-NOV-2000;
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01-DEC-2000;
20-DEC-2000;
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25-MAY-2001;
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22-JAN-2001;
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28-FEB-2001;
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09-MAR-2001;
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17-AUG-2000;
23-AUG-2000;
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1429 ACTGAATTGTCTCAGGCACCGTGCAAGGCTCTTACAAACGTGAGCTCCTTCGCCTCCT 1488	### Mail State ### Mail State ### Mail State ### British
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61 ATATGATGTCCTCATAGAAGGTGAACTGGAGGCGATGAGGCAATGTGACAAGTA 120 349 TGACGCCCAGCACCTCTCAGCCCACTGTGTCCTCTGCTGTTTGTGAT 408 121 TGACGCCCAGGCACTCTCAGCCCAGCTGGTCTCTCTGCTGTTTGTGAT 408 121 TGACGCCCAGGCAGCTCAGCCCAGCTGGTCTCTTGTGAT 180 409 CGGTGTCCTGGACAACTCTCCTGGTTGTGTTATAAAGGACTCAAACG 468 181 CGGTGTCCTGGACAATCTCCTGGTTGTGTTATCCTGGTAAAATATAAAGGACTCAAACG 240 469 CGGTGTCCTGGACAATCTCTTGTTGTTTATCCTGGTAAAATATAAAGGACTCAAACG 240 469 CGTGGAAAATATCTATCTTCTAAACTTGGCAGTTTCTTAACTTGTTTTTTTT	649 GTITITICGCAAAGGGCAACTITICCCAGCAGAGGGGGCGCCCTGGGCATCATTA (188 421 GTITITICGCAAAGGGCAACTITICCCAGCAGAGGGGGGCCCCTGGGCATCATTA (189 422 GTITITICGCAAAGGCCATTTTCCTGCCCAGAGGGGGGCCCCTGGCCCTGTGCCATTATTA (189 431 AGCTCCTGGCATGGGTAAAGCCATTTTCCAGCCACTTTAGCAGACTCCCTTCCTGCCGC (189 432 AGCTCCTGGCATGGGTAAAGCCATTTTCTCAGCTATTAGCAGAACTCCCTTCCTGCCGC (189 433 AGCTCCTGGCATGGGTAAAGCCATTTTCTCAGCTATTAGCAAACTCCCTTCCTGCCGC (189 434 AGCTCCTATTTTTTTACATTTCTCAGTTTAAAATGAACATTTCGCTTCTGCCG (189 435 CCCCTATTTATTTTTACATTTCTCAGTTTTAAAATGAACATTTCGCTTCTGCGC (189 436 CCCCCTATTTATTTTTACATTTCTCTTTTGCAATTTAAAAATGAACATTTCCGTTCTGGCG (189 437 CCCCTATTTATTTTTACATTTCTCTATTGCAATTTCAGAACTTCCCTTCTGGCG (189 438 CCCCCTATTTATTTTTACATTTCTCTATTGCAATTTCAGAACTTCCCTTCTGGCG (189 440 CCCCTATTTATTTTTACATTTCTCTATTGCAATTAGAAAAACATTTCCCTTCTGTGG (189 451 CCCCTATTTATTTTTACATTTCTCTATTGCAATTAGAAAAACACTTACCGTCTTGTGG (189 452 CCCCCTATTTATTTTTCAACTTTCCTGTCCACTTTCAAAGAACACTTCCCTTCTGTGG (189 454 CCCCCTATTTATTTTTCAAGTTTTCCTGTCCACTTTCAAAGAACACTTCCCTTCGGGG (189 455 CCCCCTATTTATTTTTCAAGTTTTTCCTGTCCACTTTCAAAGAACACTTCCCTTCGGGG (189 465 CCCCCTATTTATTTTTCAAGTTTTTCCTGTCCACTTTCAAAGAACACTTCCCTTCTGTGGG (189 466 CTGCAAGGGTATTTCCATTTTTTTTTTTTTTTTTTTTTT

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                                                                                                   GITITIGCACAAGGGGAACTITITCTCAGCCAGGAGGAGGGGGCCCTGTGGCATCATTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycoradial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver cardinoma) and wound healing. The present sequence is a coding sequence of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                       Paoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 86.5%; Score 1468.4; DB 6; Length 1475; Best Local Similarity 99.9%; Pred. No. 0; Matches 1469; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                         Gerber H, Gerritsen ME, Goddard A;
i, Hillan KJ, Marsters SA, Pan J,
EK, Williams PM, Wood WI, Ye W;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 15; 567pp; English
25-MAY-2001; 2001US-00866028.
25-MAY-2001; 2001US-00866034.
25-MAY-2001; 2001WS-0S017092.
30-MAY-2001; 2001WS-0870574.
30-MAY-2001; 2001WS-0S017443.
01-JUN-2001; 2001WS-US017600.
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J, Gurney AL, Hi
, Watanabe CK, V
                                                                                                                                                                  GODDARD A.
GODDARN P. J.
GODDARN P. J.
HILLAN K. J.
MARSTERS S. A.
PAONI N. F.
STEPHAN J. F.
WILLIAMS P. M.
WOOD W. I.
                                                                                                                                           GERBER H.
GERRITSEN M E.
                                                                                                     INC
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P-PSDB; ABB95430.
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FERRARA I
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Godowski PJ,
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The invention relates to an isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded by the nucleic acid, a polypeptide encoded by the nucleic acid, or an agonist or antagonist, is used to treat a cardiovascular, endothelial, or angiogenic disorder in a mammal, cor has cardiac hypertrophy, trauma, a cancer, or age-related macular or preferably a human. The human may have suffered a myocardial infarction or has cardiac hypertrophy, trauma, a cancer, or age-related macular can elevated level of PGF-2 alpha. A PRO polypeptide, given in the specification, or an agonist is used to inhibit or stimulate endothelial call growth in a mammal. PRO21 or an agonist is used to induce cardiac hypertrophy. PRO1376 or PRO1499 is used to stimulate angiogenesis. A PRO polypeptide, given in the specification, or an agonist is used to induce endothelial call apoptosis. A PRO selmulate or inhibit smooth muscle call growth, or to induce endothelial call and the control or stimulate or inhibit smooth muscle call growth, or to induce endothelial call and the specification or an agonist is used to call growth and the specification or an agonist or to induce endothelial call and the specification or an agonist or to induce endothelial call and the specification or an agonist or to induce endothelial call and the specification or an agonist or to induce endothelial call and the specification or an agonist or to induce endothelial call and the specification or an agonist or to induce endothelial call and the specification or an agonist or to induce endothelial call and the specification or an agonist set to induce endothelial call and the specification or to induce endothelial call and the specification or to induce endothelial call set to the specification or to induce endothelial call set to the specification or to induce endothelial call set to the specification or to induce endothelial call set to the specification or to induce endothelial call set to the specification or to
New isolated nucleic acid encoding a secreted and transmembrane polypeptide for treating a cardiovascular, endothelial, or angiogenic disorder in a mammal, such as cancer or age-related macular degeneration.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     se; gene; human; secreted protein; transmembrane protein; cardiovascular disorder; endothelial disorder; angiogenic disorder; myocardial infarction; cardiac hypertrophy; trauma; cancer; age-related macular degeneration; angiogenesis; endothelial cell apoptosis; smooth muscle cell growth; endothelial cell tube formation.
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KJ, Marsters SA, Pan J,
WI, Ye W;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted/transmembrane PRO polypeptide cDNA #8.
                                                                                                         CGACATGAAATAAATGTATTTTAAAACATC 1470
                                                                              CGACATGAAATAAATGTATTTAAAACATC
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20-JUN-2001; 2001WO-US019692.
09-JUL-2001; 2001WO-US021735.
20-FEB-2002; 2002US-00081056.
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J, Gurney AL, Hi
K, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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P-PSDB; ADD10305.
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Watanabe CK,
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86.5%; Score 1468.4; DB 10; Length 1475;

Query Match

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           1; Indels
Pred. No. 0;
0; Mismatches
 186.66
Best Local Similarity 99.9
Matches 1469; Conservative
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GJ, Marsters SA,
VI, Ye W;
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09-JUL-2001; 2001MO-US021735.
20-FEB-2002; 2002US-00081056.
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P-PSDB; ADD11265.
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Godowski PJ,
Watanabe CK,
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The invention relates to an isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded by the nucleic acid, or an agonist or antegonist, is used to treat a cardiovascular, endothelial, or angiogenic disorder in a mammal, or has cardiac disorder in a mammal, or has cancer or age-related macular degeneration. The human may have suffered a myocardial infarction or has cardiac hypertrophy, trauma, a cancer, or age-related macular degeneration. The cardiac hypertrophy is characterised by the presence of an elevated level of PGF-2 alpha. A PRO polypeptide, given in the specification, or an agonist is used to inhibit or stimulate endothelial chypertrophy. PRO1376 or PRO149 is used to stimulate angiogenesis. Chypertrophy. PRO1376 or PRO149 is used to stimulate angiogenesis. Chypertrophy. PRO1376 or paged to induce endothelial cell apoptosis. A PRO polypeptide, given in the specification, or an agonist is used to stimulate or inhibit smooth muscle cell growth, or to induce endothelial cell the endothelial cell the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 ATATGATGTCCTCATAGAAGGTGAACTGGAGGGGATGAGGCAGAGCAATGTGACAAGTA 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGAGCTCAGCCCAGTGGGCAGTCTGAAGATGGCCAATTACACGCTGGCACCAGAGGATGA
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                                                                                                                                                                                                                                                               Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J,
Watanabe CK, Williams PM, Wood WI, Ye W;
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09-JUL-2001; 2001WO-US021735.
20-FEB-2002; 2002US-00081056.
                                                                                 16-AUG-2002; 2002US-00223088
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Best Local Similarity 99.9%;
Matches 1469; Conservative
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Matches 1469; Conservative
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The invention relates to an isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded by the nucleic acid, or an agonist or antagonist, is used to treat a cardiavascular, endothelial, or angiogenic disorder in a mammal, or has cardiac hypertrophy, trauma, a cancer, or age-related macular degeneration. The human may have suffered a myocardial infarction or has cardiac hypertrophy is characterised by the presence of an elevated level of PGF-2 alpha. A PRO polypeptide, given in the specification, or an agonist is used to inhibit or stimulate endothelial chypertrophy. PRO1376 or PRO21 or an agonist is used to induce cardiac hypertrophy. PRO1376 or PRO449 is used to stimulate angiogenesis. PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO polypeptide, given in the specification, or an agonist is used to cardiac collypetide, given in the specification, or an agonist is used to cardiac cell tube formation. The present sequence represents a cDNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard A;
1, Pan J, Stephan JF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       se; gene; human; secreted protein; transmembrane protein; cardiovascular disorder; endothelial disorder; angiogenic disorder; myocardial infarction; cardiac hypertrophy; trauma; cancer; age-related macular degeneration; angiogenesis; endothelial cell apoptosis; smooth muscle cell growth; endothelial cell tube formation.
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J, Hillan KJ, Marsters P
PM, Wood WI, Ye W;
Claim 2; SEQ ID NO 15; 492pp; English.
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09-JUL-2001; 2001WO-US021735.
20-FEB-2002; 2002US-00081056.
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P-PSDB; ADE41266.
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Watanabe CK,
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Length 1475;

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Score 1468.4; Pred. No. 0; 0; Mismatches

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inducing cardiac hypertrophy, cell apoptosis or cell tube formation and stimulating angiogenesis or smooth muscle cell growth by administering polypeptides of the invention. The PRO polypeptides and polymucleotides are useful for treating cardiovascular, endothelial or angiogenic disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma, cancer or age-related macular degeneration. The PRO polymucleotides are useful as hybridisation probes in chromosome and gene mapping and in generating antisense RNA and DNA, and for chromosome identification and tissue typing. The PRO polypeptides and polymucleotides are also useful in gene therapy and as molecular weight markers for protein electrophoresis purposes. This sequence represents a human PRO polymucleotide of the invention.
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                                                                                                                                                                                                   Score 1468.4; DB 12; Length 1475;
Pred. No. 0;
0; Mismatches 1; Indels 0;
                                                                                                                                                                            Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
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Best Local Similarity 99.9%;
Matches 1469; Conservative
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98WO-US025108.
98US-00218517.
99WO-US000106.
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99WO-US005028.
99US-00254460.
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99US-00284291.
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19-NOV-1998;
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22-DEC-1998;
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02-JUN-2000;
28-JUL-2000;
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15-SEP-1999;
15-SEP-1999;
05-OCT-1999;
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01-SEP-1999;
08-SEP-1999;
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28-FEB-2001;
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09-MAR-1999;
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09-MAR-2001; 2001US-00802706

05-APR-2001; 2001US-00808689.

05-APR-2001; 2001US-00866028.

25-MAY-2001; 2001US-00866028.

25-MAY-2001; 2001US-00866034.

25-MAY-2001; 2001US-00866034.

25-MAY-2001; 2001US-00866034.

01-JUN-2001; 2001US-00892636.

19-JUN-2001; 2001US-00882636.

19-JUN-2001; 2001US-00882636.

19-JUL-2001; 2001US-00882636.

09-JUL-2001; 2001US-00918585.

09-JUL-2001; 2001US-00918585.
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30-NOV-2001; 2001US-00001054.
06-DEC-2001; 2001US-000058767.
19-DEC-2001; 2001US-00052806.
15-JAN-2002; 2002US-00052586.
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(GETH) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF; Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2004-225727/21. P-PSDB; ADK82794.

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or PRO21383, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

Claim 2; SEQ ID NO 15; 494pp; English.

The invention relates to human PRO polypeptides and the PRO polynucleotides encoding them. The invention also relates to treating cardiovascular, endothelial or angiogenic disorders in mammals, inhibiting endothelial or angiogenic disorders in mammals, inhibiting endothelial cell growth, stimulating endothelial cell growth, stimulating endothelial cell growth, stimulating angiogenesis or smooth muscle cell growth by administering polypeptides and polypeptides and polypeptides of the invention. The PRO polypeptides and polynucleotides are useful for treating cardiovascular, endothelial or angiogenic disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma, cancer or age-related macular degeneration. The PRO polypucleotides are useful as hybridisation probes in chromosome and gene mapping and in concern or age related macular degeneration. The PRO polymucleotides are also useful in gene therapy and as molecular weight markers for protein in gene therapy and as molecular weight markers for protein in gene therapy and as molecular weight markers for protein collectoride of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at equate the patent is sequence.

Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;

0; Gaps DB 12; Length 1475; 1; Indela Query Match 86.5%; Score 1468.4; Best Local Similarity 99.9%; Pred. No. 0; Matches 1469; Conservative 0; Mismatches

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Db 1081 GCAAGAAGAATAAACATGGATTTTC 29 1369 ATTTGTATACAAAATCGGATACAGG 1141 ATTTGTATACAAAATCGGATACAGG 1142 ACTGAATTTGTCTCAGGCACCGTGC 1489 ACTGAATTTGTCTAGGCACCGTGC 1489 ACCACTTGTCCATAGTCTGGATAGA 1549 ACCACTTGTCCATAGTCTGGATAGA 1549 ACCACTTGTCCATAGTCTGGATAGA 1549 ACCACTTGTCCATAGTCTGGATAGA 1549 ACCACTTGTCTAAGATCTGGATAGA 1549 ACCACTTGTCTAAGATCTGGATAGA 1549 ACCATTGTCTAAGATCACATAA 1609 AGCATTGCTCAAGACCTACGCTTG 1381 AGCATTTGCTCAGAGCCTACGCTTG 1569 AGCATTGCTCAGAGCCTACGCTTG 1569 AGCATTGCTCAGAGCCTACGCTTG 1569 AGCATTGCTCAGAGCCTACGCTTG 1569 AGCATTGCTCAGAGCCTACGCTTG 1569 AGCATTGCTCAGAGCCTACGCTTG 1669 AGCATTGCTCAGAGCCTACGCTTG 1669 AGCATTGCTCAGAGCCTACGCTTG 1669 AGCATTGCTCAGAGCCTACGCTTG 1669 AGCATTGCTCAGAGCCTACGTTTTAAA 1669 ACCATGAAATAAAATGTATTTAAA 1669 ACCATGAAATAAAATGTATTTAAAA 1669 ACCATGAAATAAAATGTATTTAAAA 1669 ACCATGAAATAAAATGTATTTAAAA 1661 ACCATGAAATAAAATGTATTTTAAAA 1661 ACCATGAAATAAAATGTATTTAAAA 1661 ACCATGAAATAAAATGTATTTTAAAA 1661 ACCATGAAATAAAATGTATTTTAAAA 1661 ACCATGAAATAAAATGTATTTTAAAA 1661 ACCATGAAATAAAATAAAATAAATTTAAAAA 1661 ACCATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	RESULT 11 AEZ42782 ID ABZ42782 XX AC ABZ42782; XX DY 04-MAR-2003 (first entry) XX DE Human chemokine receptor-like 2 nuu XX XX DE Human chemokine receptor-like 2 nuu XX X	PN WO200261087-A2. XX PD 08-AUG-2002. XX PS 19-DEC-2001; 2001WO-US050107. XX PR 19-DEC-2000; 2000US-0257144P. XX (LIFE-) LIFESPAN BIOSCIENCES INC. XX PI Burmer GC, Roush CL, Brown JP; XX PY PSDB; ABP81334. PF PSDB; ABP81334. YX New isolated antigenic peptides e.; PT (GPCR), useful for diagnosing and in which GPCRs are involved, e.g. XX XX PT autoimmune diseases. XX PSSB; Disclosure; Fig 1; 523pp; English. XX PSSB; English.
		1009 GGGCCCTACAATATTGCATTTTCCTGTCCACTTTCAAAGAACACTTCTCCCTGAGTGA 1068 781 GGCGCCCTACAATATTGCATTTTTCCTGTCCACTTCAAAGAACACTTCTCCCTGAGTGA 840 1069 CTGCAAGAGCACAATATTGCATTTTTCAAAGAACACTTCTCCCCTGAGTGA 840 1069 CTGCAAGAGCACTACAATCTGGACAAAAGTGTTCACATCACTCATCGCCACCAC 1128 841 CTGCAAGAGCACTACAATCTGGACAAAAGTGTTCATCACTCAAAACTCATCGCCACCAC 900 1129 CCACTGCTGCATCAACTCTCTGATGGGACATTTAGCAAATACCT 960 1189 CTGCCGCTGTTTCCATCTGGCGTAGCGTTTCTTGATGGGACATTTAGCAAATACCT 960 1189 CTGCCGCTGTTTCCATCTGCGTAACACCCCCTTTCAACGGGGGGGG
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibody against a particular GPCR, and in the production of specific contibods. The peptides and antibodies are useful for disgnosting and designing drugs for GPCRs and antibodies are useful for disgnosting and designing drugs for GPCRs and antibodies are useful for disgnosting and designing drugs for creating immune-related disease, immunological-related disease, cell proliferative diseases, or autoimmune diseases, growth-related disease, cancering in a section or viral infections, atherosclerosis, bacterial, fungal, protozoan or viral infections, of setoatthrities, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophremia, dementia, mental retardation, memory and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                loss, epilopsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPGKB are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention
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Sequence 1645 BP; 443 A; 383 C; 361 G; 458 T; 0 U; 0 Other

1645; 0; Gaps 0;	AATATGATGTC 298	HIIIIIIIII BATATGATGTC 244	ATGACGCCCAG 358	HIIIIIIIIII	ATCGGTGTCCTG 418		GCGTGGAAAAT 478		TGCCCTTCTGG 538		TCGTGGCCTG 598	TCGTGGGCCTG 544	TGTTTTGCAC 658	HGTTTTTGCAC 604	CAAGTGTCCTG 718		AACCTCAGATG 778	AACCTCAGATG 724	CTGATGAGACA 838	CTGATGAGACA 784	000 ###
Score 1455.2; DB 8; Length 1645; Pred. No. 0; 0; Mismatches 3; Indels 0;	CCAGTGGCAGTCTGAAGATGGCCAATTACACGCTGGCACCAGAGGATGATATGATCTC		CTCATAGAAGGTGAACTGGAGAGCGATGAGGCAGGCAATGTGAGCAATGAGGCAGG	CTCATAGAAGGTGAACTGGGAGGGGGGGGGGGGATGTGAGGGAGG	GCACTCTCAGCCCAGCTGCCATCACTCTGCTGTGTTTTGTGATCGGTGTCTTG	GCACTCTCAGCCCAGCTGGTGCCATCTCTCTGCTGCTGTTTTTTTT	GACAATCTCCTGGTTGTGCTTATCCTGGTAAAATATAAAGGACTCAAACGCGGGGAAAAT	GACAATCTCCTGGTTGTGCTTATCCTGGTAAAATATAAAGGACTCAAACGGGAAAAT	ATCTATCTTCTAAACTTGGCAGTTTCTAACTTGTGTTTTCTTGCTTACCCTGCCCTTCTGG	ATCTATCTTCTAAACTTGGCAGTTTCTAACTTGTGTTTCTTGCTTACCCTGCCCTTGTGG	GCTCATGCTGGGGGGGGATCCCCATGTGAAAATTCTCATTGGACTGTACTTCGTGGGCCTG	GCTCATGCTGGGGGGGATCCCATGTGTAAATTCTCATTGGACTGTACTTCGTGGGCCTG	TACAGTGAGACATTTTTCAATTGCCTTCTGACTGCGAAAGGTACCTAGTGTTTTTGCAC	TACAGTGAGACATTTTTCAATTGCCTTCTGACTGTGCAAAGGTACCTAGTGTTTTTGCAC	AAGGGCAACTTTTTCTCAGCCAGGAGGGGGGGGCCCTGTGGCATCATTACAAGTGTCCTG	-	GCATGGGTAACAGCCATTCTGGCCTCAATACGTGGTTTATAAACCTCAGATG	GCATGGGTAACAGCCATTCTGGCCACTTTGCCTGAATACGTGGTTTATAAACCTCAGATG	GAAGACCAGAAATACAAGTGTGCATTTAGCAGAACTCCCTTCCTGCCAGGTGATGAGACA	GAAGACCAGAAATACAAGTGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACA	りょう 一番出来 まかいいくい まんしゅう はいかい はんしょく まんかい きょく ちょうしん かいかい しゅうしゅう しゅうしゅ しゅうしゅ しゅうしゅ しゅうしゅ しゅうしゅう しゅうしゃ しゅうしゅう しゅうしゅう しゅうしゅう しゅうしゃ しゅうしゃ しゅうしゅう しゅうしゃ しゅん しゅうしゅん しゅん しゅん しゅん しゅん しゅん しゅん しゅん しゅん しゅん
85.7%; 99.8%; vative			_						-		-									GAAGACCAGAAATACAAGTGTGC	
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This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic composition comprises contacting man agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises and with a mutation in at case one allele of a gene encoding a LEC protein, where the mutation in at least one allele of a gene encoding a LEC protein, where the mutation in a correlates with lymphoedema in human subjects, and with the proviso that composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polymucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic, vasotropic or antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary lymphoedema, in screening for an endothelial cells, in treating hereditary cyclopicament for the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the treatment of the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation. The lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation. The lymphatic growth agent may also be used in manufacturing a compact or of other diseases and cancer metastasis via the lymphatic compact or of other diseases and cancer metastasis via the lymphatic compactors. The present sequence is that of a human LEC/BEC differentially experient sequence is that of a human LEC/BEC differentially experient sequence does not appear in the specification
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vasotropic, antiinflammatory; gene therapy; endothelial cell disorder; inflammatory disease; cancer metastasis; lymphatic system; gene; ds;
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                                                                                                                                                                                                                                                                                                                                                                                      Saharinen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 653; 176pp; English
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                                                                                                                                                                                                                                                                                                                  CANCER RES
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Matches 1457; Conservative
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(LICN ) LICENTIA LTD
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1384 1504 964 658 718 868 484 544 604 664 778 724 838 784 ATTITIACATTITCICTATGIGCAAATGAGAAAAACACTAAGGTICAGGGAGCAGAGGTAT 958 AAGGGCAACTITITCTCAGCCAGGAGGAGGCTCCTGTGGCATCATTACAAGTGTCCTG 125 GAAGACCAGAAATACAAGTGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACA GCTCATGCTGGGGGGGGATCCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTG TACAGTGAGACATTTTTCAATTGCCTTCTGACTGTGCAAGGTACCTAGTGTTTTTGCAC GCATGGGTAACAGCCATTCTGGCCACTTTGCCTGAATACGTGGTTTATAAACCTCAGATG 1205 AGGGAAGAACCTGACCATTCCACCGAAGTGTAAACTAGCATCCACCAAATGCAAGAAGAA TAAACATGGATTTTCATCTTTTCATTTTTCATGTAAATTTTCTACACTTTGTATAC 1445 CATAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAGAAAACTAAGGCGGGAAATTTG GACAATCTCCTGGTTGTGCTTATCCTGGTAAAATATAAAGGACTCAAACGCGTGGAAAAT ATCTATCTTCTAAACTTGGCAGTTTCTAACTTGTGTTTTCTTGCTTTACCCTGCCTTTCTGG GCTCATGCTGGGGGCGATCCCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTG ATTITTACATTTCTCTATGTGCAAATGAGAAAAACACTAAGGTTCAGGGAGCAGAGGTAT AATATTGCATTTTTCCTGTCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGC TTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACAAGGCACATCG AGGGAAGAACCTGACCATTCCACCGAAGTGTAAACTAGCATCCACCAAATGCAAGAAA AAAATCGGATACAGGAAGAAAAAGGGAGAGAGGTGAGCTAAACATTTGCTAAGCACTGAATTTG 1385 rereadscaccerscandscreitracanacersacerscreecerscenesacers CATAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAAACTAAGGCGCGGAAATTTG ATCTATCTTCTAAACTTGGCAGTTTCTAACTTGTGTTTCTTGCTTACCCTGCCCTTCTGG AAGGCCAACTTTTCTCAGCCAGGAGGGTGCCCTGTGCCATCATTACAAGTGTCCTG GCATGGGTAACAGCCATTCTGGCCACTTTGCCTGAATACGTGGTTTATAAACCTCAGATG GAAGACCAGAAATACAAGTGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACA TTCTGGAAGCATTTTCTGACTTTAAAAATGAACATTTCGGTTCTTGTCCTCCCCCTATTT AATATTGCATTTTTCCTGTCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGC ATCAACCCTCTCCTGTATGCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGT TACAGTGAGACATTTTCAATTGCCTTCTGACTGTGCAAAGGTACCTAGTGTT 545 1019 1079 1139 1085 1199 1259 1319 1265 1379 1325 1439 1499 425 539 485 599 629 605 719 665 839 785 899 845 959 905 965 479 779

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated nucleic acid and the PRO
polypeptide encoded by it. A protein of the invention has
antinifiammatory, antilarthritic, antirheumatic, immunosuppressive,
corecopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
cof the invention may have a use in gene therapy. The PRO polypeptide, its
cof the invention may have a use in gene therapy. The PRO polypeptide, its
cagonist, antagonist, or antibody that specifically binds to the
polypeptide is useful for treating an immune related disorder such as
colypeptide is useful for treating an immune related disorder such as
systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
idvopathic inflammatory myopathy, Sjogren's syndrome, systemic
clopathic inflammatory myopathy, Sjogren's syndrome, systemic
thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
disease, a demyelinating disease of the central or peripheral nervous
system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
cof elecancy demyelinating polyneuropathy, Guillain-Barre syndrome,
disease, infectious or autoimmune chronic active hepatitis, primary
clisease, infectious or autoimmune chronic active hepatitis,
chiliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
                                                                                        1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 new PKO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immuné-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system.
                                                                                                                                                                                                                                                                                                             ss; gene; PRO; antinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
                                                                             CAGAGCCTACGCTTGGTCCAGAACATCCAAACTCCAAACCCTGGGGACAAACGACATGAAA
                                   TCTAAGATCACATAACTAGGAAGTGGCAGAACTGATTCTCCAGCCCTGGTAGCATTTGCT
                                                            CAGAGCCTACGCTTGGTCCAGAACATCAAACTCCAAACCCTGGGGACAAACGACATGAAA
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                                                                                                                                                                                                                                                                                        polypeptide encoding cDNA SEQ ID NO:1620.
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                                                                                                               TAAATGTATTTTAAAACATC 1698
                                                                                                                                         TAAATGTATTTTAAAACATC 1644
                                                                                                                                                                                                           standard; cDNA; 1645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002US-0423394P
                                                                                                                                                                                                                                                              (first entry)
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P-PSDB; ADP24443.
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                     disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung eosinophilic pneumoniay fibrosis, hypersensitivity pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence encodes a PRO protein of
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                                                                                                                                                                                                                                                                                                                                       Gape
or immune-mediated skin disease, a bullous
                                                                                                                                                                                                                                                                                 Length 1645;
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                                                                                                                                                                                                                              BP; 443 A; 383 C; 361 G; 458 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                 DB 13;
                                                                                                                                                                                                                                                                               Score 1455.2;
Pred. No. 0;
0; Mismatches
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Best Local Similarity
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1445 CATAGTGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAACTAAGGCGCGGAAATTTG 1504
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                                      1085 ATCAACCCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAATACCTCTGCCGCTGT
                                                                                        1145 TTCCATCTGCGTAGTAACACCCCACTTCAACCCCAGGGGGCAGTCTGCACAGGCACATCG
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This invention relates to a novel method for determining whether an individual is predisposed to inflammatory bowel disease (IBD), preferably to ulcerative collitis. Specifically, it refers to the identification of single nucleotide polymorphisms (SNPs) in the CCRL2 polymucleotide or chemokine (C-C motif) receptor—like 2 protein that is also known as HCR. The present invention describes methods for preventing or treating IBD, as well as diagnosing a predisposition to the disease by use of probes, primers and antibodies that can detect and amplify the CCRL2 SNP regions. Furthermore, it provides a screening assay for agents that can be used to identify individuals with a genetic predisposition and in turn be used for gene therapy purposes. The pharmaceutical compositions derived for gene therapy purposes. The pharmaceutical compositions derived for generic six the human CCRL2 cDNA of the invention. NOTE: This sequence sequence is the human CCRL2 cDNA of the invention. NOTE: This sequence
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                                                                                              Determining whether an individual is predisposed to inflammatory bowel disease (i.e. ulcerative colitis) comprises identifying whether the individual has a polymorphism in the CCRL2 polynucleotide or protein.
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Human pulmonary and inflammatory target DNA #259 BP. DNA; 143040 (first entry) ABD20648 standard; 29-JUL-2004 ABD20648 RESULT 15 2 ******

respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallersic; antiinflammatory; antiastmatic; analysesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis; beta adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory diserses syndrome; allersic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ds. ä Aguilar Pabalan J, щ Katz ŝ Li Y, Sandrasagra A, Tang L, Shahabuddin 23-APR-2002; 2002WO-US013143. 24-APR-2001; 2001US-0286036P. (EPIG-) EPIGENESIS PHARM INC. WPI; 2003-093058/08. WO200285309-A2. Homo sapiens 31-OCT-2002 Nyce JW, 1 Miller S,

Pharmaceutical composition for treating asthma, has antisense oligonuclectide containing less percentage of adenosine, targeted toucleic acids associated with lung airway or lung dysfunction, and Claim 15; SEQ ID NO 12041; 763pp; English nucleic acids associat bronchodilating agent.

This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating comprising oligonucleotides, effective for alleviating comprising oligonucleotides, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating content of a target polypeptide associated with lung airway or lung airwaton or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antinflammatory, antiasthmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or maligant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or bronchoconstriction and/or lung or administered composition, and/or bronchoconstriction, respiratory distress syndrome, pain, cystic fibrosis, allergic rhintis, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to the oligonucleotides into products that free adenosine into the system composition and unwanted effects due to it the adenosine into the system composition and unique to it the eligonucleotides into product of the cit in the target RNA serves to prevent the breakdown of the edgradation and unique to it in the target RNA serves to prevent any u

G; 39343 T; 0 U; 0 Other; Sequence 143040 BP; 41190 A; 30113 C; 32394

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CCAGTGGGCAGTCTGAAGATGGCCAATTACACGCTGGCACCAGAGGATGAATATGATGTC

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ò	659 A	AAGGGCAACTITITCTCAGCCAGGAGGAGGGGCCCTGTGGCATTACAAGTGTCCTG 718
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ò	899 A7	ATTITIACATITCTCTATGTGCAAATGAGAAAAACACTAAGGTTCAGGGAGCAGGGGTAT 958
QQ	97284 AT	ITTTIACATTTCTCTATGTGCAAATGAGAAAACACTAAGGTTCAGGGAGCAGAGGTAT 97343
È	959 AC	AGCCTTTCAAGCTTGTTTTTGCCATAATGGTAGTCTTCCTTC
ор	97344 AC	SCCTITICAAGCITGITTITGCCATAATGGTAGTTCTTTCTGATGTGGGCGCCCTAC 97403
ò	1019 A	AATATTGCATTTTTCCTGTCCACTTTCCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGC 1078
qq	97404 A	ATATIGCATITITICCTGTCCACTITICAAAGAACACTICTCCCTGAGIGACTGCAAGAGC 97463
ò	1079 AC	AGCTACAATCTGGACAAAAGTGTTCACATCACTAAACTCATGGCCACCCAC
QΩ	97464 AC	SCTACAATCTGGACAAAAGTGTTCACATCACTAAACTCATCGCCACCACCACTGCTGC 97523
ò	1139 AT	ATCAACCCTCTCCTGTATGCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGT 1198
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ò	1199 TT	TTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCAACGCACATCG 1258
qq	97584 T	TGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGC
ò	1259 AC	GGGAAGAACTGACCATTCCACCGAAGTGTAAACTAGCATCCACCAAATGCAAGAAA 1318
ପ୍ପ	97644 AC	SGGAAGAACCTGACCATTCCACCGAAGTGTAAACTAGCATCCACCAAATGCAAGAA 97703
à i	319	37
g G	97704 TA	AAACATGGATTTTCATCTTTCTGCATTATTTCATGTAAATTTTCTACACATTTGTATAC 97763

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98063	98004 CAGAGCCTACGCTTGGTCCAGAACATCAAACCCCAGAGCCTGGGGACAAACGACATGAAA 98063	98004	셤
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97823	97764 AAAATCGGATACAGGAAGGAAGGGAGAGGTGAGCTAACATTTGCTAAGCACTGAATTTG	97764	g
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                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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B1819787.1 G1:15931337
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                          CTGAGCTCGGTGAGTGGGCGGCTAGAGCCACCAGGTGAAGTCAACACAGTGTTTCTCGGTG
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                                                               CTGAGCTCGGTGAGTGGGGGGGTAGAGCCACCAGGGGAA-TCAACAGTGGTTTCTCGTG
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                                                                                                                                                    397 TGTGTTTGTGATCGGTGTCCTGGACAATCTCCTGGTTGTGCTTATCCTGGTAAAATATAA 456
121 TGTGTTTGTGATCGGTGTCCTGGACAATCTCCTGGTTGTGCTTATCCTGGTAAAATATAA 180
                                                                                                                                                                                                                                                  ATGTGACAAGTATGACGCCCAGGCACTCTCAGCCCAGCTGGTGCCATCACTCTGCTCTGC 396
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                                                              Score 737.8; DB 5;
Pred. No. 3.4e-204;
0; Mismatches 22;
Technologies."
                                                              Query Match
Best Local Similarity 96.5%;
Matches 850; Conservative
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/dev_stage="adult, 16 yr"
/lab.host="wluth."
/lab.host="wluth.0s"
/clone_lib="Lupski sympathetic trunk"
/clone_lib="Lupski sympathetic lib-
/clone_lib="Lupski site_lib-
/clone_lib="Lupski si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ892457
AGENCOURT 8415422 Lupski sympathetic_trunk Homo sapiens cDNA clone IMAGE:6192227 5', mRNA sequence.
BQ892457
BQ892457.1 GI:22284471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM13593 row: o column: 12
High quality sequence stop: 601.
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                                 CATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTACAGTGAGACATTTTTCAA
                                                                                                                               CAGGAGGAGGGTGCCCTGT-GGCATCATTACAAGTGTCCTGGCATGGGTAACAGCCATTC
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mol_type="mRNA"
Lb xref="taxon:9606"
/clone="IMAGE:6192227"
/sex="male"
              CATGTGAAATTCTCATTGGA
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//IDD NOSE="WILD GLADE MACCOPRAGES challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage)
//IDD NOSE="WILD NOSE"
//IDD NOSE="WILD NOSE="WILD NOSE"
//IDD NOSE
//IDD NOS
                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CONA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
thtp://genome.uiowa.edu/distribution/cgap.html
Seg primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 729)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/mol_type="mRNA"
/db xref="taxon:9606"
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/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
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40.6%; Score 689; DB 6; L
Best Local Similarity 99.7%; Pred. No. 6.3e-190;
Matches 711; Conservative 0; Mismatches 0;
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TAG_SEQ=GGCCATGCCG"
                                     GI:31154677
                                                                                             Homo sapiens (human)
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                                  CD370587.1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.
E. (Dasses 1 to 716)
INTH-MGC http://mgc.nci.nih.gov/.
INTH-MGC http://mgc.nci.nih.gov/.
In Onpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-romail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The 1.M.A.G.E. Consortium
CDNA Library Arrayed by: The 1.M.A.G.E. Consortium
CDNA Library Arrayed by: Agencourt Bioscience Corporation
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GGGTGCCCTGTGGCATCATTACAAGTGTCCTGGCATGGGTAACAGCCATTCTGGCCACTT
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Pred. No. 8.2e-188;
0; Mismatches 22;
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Best Local Similarity 96.7%;
Matches 728; Conservative
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                                                                                                  /organism="Homo sapiens"
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For information about which gene each clones represents, please visit our anonymous ftp site at tip://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NIH_MGC Library."
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Clone distribution: MGC clone distribution information can l found through the I.M.A.G.E. Consortium/LLNL at: http://image.lln.gov
Plate: IRB102 row: f column: 06
High quality sequence stop: 634.
Location/Qualifiers
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Best Local Similarity 98.9
Matches 703, Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases I to 750)

2. Unpublished (1999)

3. National Institutes of Health, Mammalian Gene Collection (MGC)

3. National Institutes of Health, Mammalian Gene Collection (MGC)

4. Unpublished (1999)

5. Contact: Robert Strausberg, Ph.D.

5. Email: cgapbs-r@mail.nih.gov

7 Issue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CLONG distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Linng the Library Sequence of Column: 11

High quality sequence stop: 735.

Liocation/Qualifiers BE871331 750 bp mRNA linear EST 20-OCT-2000 601449442F1 NIH MGC_65 Homo sapiens cDNA clone IMAGE:3853378 5', TTTATTTCAGTTGGTCCCTGAGCTCGGTGAGTGGGGCGGGTAGAGCCACCAGGGGAATCA 106 166 61 ACAGIGGITICICGIGCCCCTCAGGGCAGCAGTCTGATCAAAAGGAGGGCATCCAC 120 226 180 286 406 ACAGTGGTTTCTCGTGCCCCTCAGGGTCAGGAGCAGTCTGATCAAAAGGAGGGCATCCAC 121 TGTCCGGGGCCATTCCCACAGCTCCCGGATGCTGGGTCTGGAGGCTGCGCCCTTCCCCTG GAATATGATGTCCTCATAGAAGGTGAACTGGAGAGCGATGAGGCAAGAGCAATGTGACAAG CAGGAGCTCAGCCCAGTGGGCAGTCTGAAGATGGCCAATTACACGCTGGCACCAGAGGAT 3; Gaps 954 Length 750; IndelB

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
California, Berkeley) using ZAP-cDNA synthesis Kit (Stratagene) and Superscript II RT (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                    AGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCCAGGCACTCTCAGCCCCAGCTGG
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AGENCOURT 14369985 NIH MGC 191 Homo sapiens CDNA clone
IMAGE:30409698 5', mRNA sequence.
CD520843
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                                                                                         Score 646.4; DB 4;
Pred. No. 2.2e-177;
0; Mismatches 31;
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/clone into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
innert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
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1. (Jabase 1 to 773)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

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Office of Cancer Genomics

National Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.ini,gov

Tissue Procurement: Guthrie cDNA Resource Center cDNA Library Preparation: Guthrie cDNA Resource Center cDNA Library Preparation: Guthrie cDNA Resource Center cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation cloud through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

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High quality sequence start: 18

High quality sequence story: 530.
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S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

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Email: cgapbs-r@mail.nlh.gov

Tissue Procuremen: Narayan Bhat

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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High quality sequence stop: 497.

Location/Qualifiers

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Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 111-1118 (2004)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                    CCCACAGCTCCCGGATGCTGGGTCTGGAGGCTGCGCCCTTCCCCTGCAGGAGCTCAGCCC
                                                     /clone="MPE01252"
/cell_type="macrophage"
/clone_lib="Sugano cDNA library, macrophage"
                                                                                                                        Query Match 34.2%; Score 581; DB 5; Length 581; Best Local Similarity 100.0%; Pred. No. 2.6e-158; Matches 581; Conservative 0; Mismatches 0; Indels
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    .581
    /organism="Homo sapiens"
/mol_type="mRNA"
    /db_xref="taxon:9606"

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BP300486.1 GI:52229446
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to SB1)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S..
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 111-1118 (2004)
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                                                        670 TITCICAGCCAGGAGGAGGCTGCCCTGTGGCATCATTACAAGTGTCCTGGCATGGGTAAC
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                             Gaps
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  773;
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yauzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
  Length
                             Indels
Score 597.6; DB 7;
Pred. No. 4e-163;
0; Mismatches 8;
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Best Local Similarity 98.6%;
Matches 612; Conservative
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AW300833 S73 bp mRNA linear EST 18-JAN-2000 xk06g97.x1 NCI CGAP CO19 Homo sapiens cDNA clone IMAGE:2665980 3' similar to TR:\(\tilde{0}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\(\tilde{1}\)0042\
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                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MRD60730"
/call_type="macrophage"
/clone_lib="Sugano cDNA library, macrophage"
         Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzuki@ima.u-tokyo.ac.jp.
Location/Qualifiers
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Pred. No. 3.2e-150;
0; Mismatches 1;
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Best Local Similarity 99.8%;
Matches 554; Conservative 0
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Homo sapiens
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 581)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minacku, Tokyo 108-8639, Japan
Email: ysuzukideims.u-tokyo.ac.jp.
Location/Qualifiers
1. .576
/ organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="texon|5666"
/clone="MRB09014"
/cell_type="maczophage"
/clone_lib="Sugano cDNA library, macrophage"
                                                                                                                                                                                                                                                                                                                                                                                ;
0
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33.8%; Score 573.4; DB 5; Length 576;
Best Local Similarity 99.7%; Pred. No. 4.4e-156;
Matches 574; Conservative 0; Mismatches 2; Indels 0
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M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 630 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 442.
                                                                                                                                                                                                                                                           tb96a06.x1 NCI CGAP CO16 Homo sapiens cDNA clone IMAGE:2062162 3' similar to TR:000421 CCR6. ;, mRNA sequence.
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547 TATGCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGTTTCCATCTGCGTAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
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                                                                                   CGACATGAAATGTATTTTAAAACATC 1698
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                                                                                                                33 CGACATGAAATAAATGTATTTTAAAACATC
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al Similarity 99.3%;
543; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="tMAGE:2665980"
/tissue_type="moderately differentiated adenocarcinoma"
/tab.host="moderately differentiated adenocarcinoma"
/tlob host="moderately differentiated adenocarcinoma"
/clone="tMAGE:2665980"
/clone="organism="total"
/clone="organism="total"
/note="organism="total"
/note="organism="tota
                                                                                                                                                                                                                                               Email: cgapbs-remail.nib.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llhl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 401.
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                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 573)
                                                                                      1 (bases 1 to 573)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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1391
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1 (bases 1 to 517)
Bloecker, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
EST (Bloecker, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., et al.)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                              248
                                308
                                                                                                                                                                                                                                         187 GGACTAGTCTCATTTCTCTGAGAAAACTAAGGCGCGGAAATTTGTCTAAGATCACAT 128
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/mol_type="mRNA"
/do_tref="taxon:9606"
/dore="DKEPES616218"
/dov_stage="adult"
/lab_host="DH108"
/clone_lib="666 (synonym: hlcc3)"
/note="vector: pTriplEx2; Stte_1: SfilA; Site_2: SfilB; cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Wolecular Genome Analysis, German Cancer
Research Center (DKF2); Enail 8. Wiemann@dkfz- heidelberg de;
sequenced by GBF (National Research Centre for Biotechnology Ltd
Braunschweig/Germany) within the cDNA sequencing consortium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            German Genome Project.

No 81 sequence available.

This clone (DKFZp686I16218) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
TCATCTTTCTGCATTATTTCATGTAAATTTTCTACACATTTGTATACAAATCGGATACA
                  367 TCATCTTTCTGCATTATTTCATGTAAATTTTCTACACATTTGTATACAAAATCGGATACA
                                                                 GGAAGAAAAGGGAGAGGTGAGCTAACATTTGCTAAGCACTGAATTTGTCTCAGGCACCGT
                                                                                      307 GGAAGAAAAGGGAGAGGTGAGCTAACATTTGCTAAGCACTGAATTTGTCTCAGGCACCGT
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Pred. No. 2e-128;
0; Mismatches 6
Query Match
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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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June 18, 2005, 15:19:56; Search time 306 Seconds (without alignments) 9079.732 Million cell updates/sec
OM nucleic - nucleic search, using sw model
                                                        Run on:
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AF014958 1698 1 AGACGCTICAGAGATCCTCT.....TAAATGTATTTTAAAACATC 1698 Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1202784 segs, 818138359 residues Searched:

2405568 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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6: /cgn2_6/ptodata1/ina/PCTUS_COMB.seq:* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Sequence 11, Appl		1, A	Sequence 308, App	Ф	_	m	967	12,	1104		-	ť	٦,	٦,	~	Sequence 2, Appli	7	13,	Ä	95	٦,	Sequence 3, Appli	47	14	۲,	Sequence 2, Appli
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& . Query Match	85.3	74.7	57.8	35.2	13.7	13.7	13.6	13.6	13.6	13.6	13.6	13.6	13.6	٠	13.6	•	13.6	٠	•	•	•	•	•	•	•		11.6
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ALIGNMENTS

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73 GGCAGTCTGAAGATGGCCCAATTACACGCTGGCACCACAGGGATGAATATGATGTCTCTTATA 132
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                 Sequence 11, Application US/10039659A
| Patent No. 672320
| GENERAL INFORMATION:
| APPLICANT: Wang, Wei
| APPLICANT: Schall, Thomas J.
| APPLICANT: Schall, Alain P.
| PRIOR PILING DATE: 1997-07-03
| PRIOR PELING DATE: 1996-07-05
| PRIOR PILING DATE: 1996-10-11
| PRIOR FILING DATE: 1996-10-11
| PRIOR PELING DATE: 1996-10-11
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (49)..(1116)
OTHER INFORMATION:
US-10-039-659A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
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LENGTH: 1547
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138 AGCAGTCTGATCAAAAGGAGGGCATCCACTGTCCGGGGCCATTCCCACAGCTCCCGGATG 197
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GIGGATAGGACTAGTCTCTCTCAGAAGAAAACTAAGGCGGGGAAATTTGTCTAAG
                                                                                                                                                    1 TGGGGCGGGTAGAGCCACCAGGGGAATCAACAGTGGTTTCTCGTGCCCCTCAGGGTCAGG
                                                                 ATCACTTAACTAGGAAGTGGCAGAACTGATTCTCCAGCCCTGGTAGCATTTGCTCAGAGC
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                           Sequence 756, Application US/09016434

| Patent No. 6500938
| GENERAL INFORMATION:
| APPLICANT: Janice Au-Young
| APPLICANT: Janice Au-Young
| APPLICANT: Jeffrey J. Seilhamer
| TITLE OF INVENTION: COMPOSITION POR THE DETECTION OF SIGNALING
| TITLE OF INVENTION: PATHWAY GENE EXPRESSION
| NUMBER OF SEQUENCES: 1490
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
| STREET: 3174 PORTER DRIVE
| CITY: PALO ALTO
| STATE: CALIFORNIA
| COUNTRY: USA
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MEDIUM TYPE: Flopy disk

COMPUTER IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WARD PC-COS/MS-DOS

SOFTWARE: WARD PC-COS/MS-DOS

SOFTWARE: WARD PC-CASICATION DATA:

APPLICATION NUMBER: US/09/016,434

FILING DATE: HEREWITH

CLASSIFICATION DATA:

APPLICATION NUMBER: 37,09/016,434

FILING DATE: FILING PARE:

FILING DATE: FILING PARE:

FILING DATE: FILING NUMBER:

FILING DATE: FILING NUMBER:

FILING DATE: FILING DATA:

APPLICATION NUMBER: 37,071

REGISTRATION NUMBER: 37,071

REGISTRATION NUMBER: 37,071

RELEPHONE: (650) 845-0456

INFORMATION FOR SEQ ID NO: 756:

SEQUENCE CHARACTERISTICS:

LENGTH: 1270 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 1268; DB
; Pred. No. 0;
1; Mismatches
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Best Local Similarity 99.8<sup>3</sup>
Matches 1268; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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CLONE: 442279
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                                                                                       CTTCTAAACTTGGCAGTTTCTAACTTGTGTTTCTTGCTTACCCTGCCCTTCTGGGCTCAT
                                                                                                                                                                                                 GCTGGGGGCGATCCCATGTGTAAAATTCTCATTGGACTGTACTTCGGGCCTGTACAGT
                                                                                                                                                                                                                                                                                  433 GAGACTITITICAATITGCCTTCTGACTGTGCAAAGGTACCTAGTGTTTTTGCACAAGGGC
                                                                                                                                                                                                                                                                                                                                                                       493 AACTITITCTCAGCCAGGAGGAGGTGCCCTGTGGCATTACAAGTGTCCTGGCATGG
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                                CTCCTGGTTGTTGTTATCCTGGTAAAATATAAAGGACTCAAACGCGTGGAAAATATCTAT
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1855 AIGGAITITCAICITICIGCAITAITICAIGIAAATITICIACACAITIGIATACAAAAT 424
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                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: Word Perfect 6.1 for Windows/MS-DOS 6.2

SOCHTARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

SOCHTARE: WORD DATA:

APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH

CLASSIFICATION: NUMBER:

FILING DATE: REPENTER:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION NUMBER:

FILING DATE:

CLASSIFICATION NUMBER:

FILING DATE:

CLASSIFICATION:

MAME: Zeller, Karen J.

REFERENCE/DOCKET NUMBER: 37,071

REPERENCE/DOCKET NUMBER: 37,071

RELEPHONE: (650) 845-4166

INNOMMATION FOR SEQ 10

SEQUENCE CHARACTERISTICS:

LENGTH: 620 base pairs

TYPE: nucleic acid

STRANDEDIATE SOURCE:

INMEDIATE SOURCE:

LIBRARY: LUNGONTIO

CLONE: 11378524

US-09-023-655-308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.2%; Score 597.8; DB 4; 99.2%; Pred. No. 1.1e-179; ive 0; Mismatches 4;
                 ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.2
Matches 610; Conservative
CORRESPONDENCE ADDRESS
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; Sequence 308, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart;
APPLICANT: Jeffrey J. Seilhamer
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
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larity 56.8%; Pred. No. 3.2e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTCAGCCAGGAGGAGGGTGCCCTGTGGCATCATTACAAGTGTCCTGGCATGGGTAACAG 731
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                                                                                                           Mary Brawner, and Usman Shabon 6388055el Mouse Genomic Clone of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1059
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                                                                                                                                                                                                                                                                                                                            ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486 ...... AND WARROUDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 230.6; DB : Pred. No. 1.9e-62
                                                                                                                                                                                                                       8: SmithKline Beecham Corporation 709 Swedeland Road, P.O. Box 1539
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/724,984A FILING DATE: October 3, 1996 CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                       APPLICANT: Derk Bergema, Mary Braw
TITLE OF INVENTION: CKR5 Receptor
WUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
RESULT 7
US-08-724-984A-3
'Sequence 3, Application US/08724984A
'Patent No. 6388055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: William T. Han
REGISTRATION NUMBER: 34,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: AT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INCORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 522; Conservative
                                                                                                                                                                                                                                            STREET: 709 Swedelauu
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Linear
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Best Local Similarity
                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   USA
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1023 TTGCATTTTTCCTGTCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCT 1082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 cegadecerioceaaaaareaareraadeaadeaaareecadecedecereerederere 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 acticactecitiricatertriegitrirericeccaacarecteciteatectectearicataa 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATATAÀAGGACTCAAACGCGTGGAAAATATCTATCTTCTAAACTTGGCAGTTTCTAAACT 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||| ||| | | ||| | | |||| | |||||||||| || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || || |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      crefertrecercicicededarcarcritaceagarcreadadedacercreari 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     784 Triercerrericandacerrecadantrerragecercantarrecagnáceren 843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                912 TCTATGTGCAAATGAGAAAACACTA-----AGGTTCAGGGAGCAGAGGTATAGCC 962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.6%; Score 230.6; DB 4; Length : 57.0%; Pred. No. 2.1e-62; ive 0; Mismatches 354; Indels
     REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                            967:
                                                                                                                                                                                         TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               LENGTH: 1225 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.6
Best Local Similarity 57.0
Matches 522; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
FIMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 91502408
US-09-023-655-967
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
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APPLICANT: Cocke, Benjamin G. APPLICANT: Cocke, Benjamin G. APPLICANT: Susan G. Stuart: APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: EXPRESSION NUMBER OF SEQUENCES: 1508 CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: PALO ALTO STREET: CALIFORNIA COUNTRY: USA
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APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
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j Sequence 1104, Application US/09016434
j Sequence 1104, Application US/09016434
j Patent No. 6500938
j GENERAL INFORMATION:
j APPLICANT: Jainice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
j TITLE OF INVENTION: PATHWAY GENE EXPRESSION
j VUMBER OF SEQUENCES: 1490
j CORRESPONDENCES: 1490
j CORRESPONDENCES: INCYTE PHARMACEUTICALS, INC.
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STREET: 3174 PORTER DRIVE
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                               RESULT 9
US-09-087-222A-12
Sequence 12, Application US/09087232A
| Sequence 12, Application US/09087232A
| Patent No. 6155431
| GENERAL INFORMATION:
| TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
| TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION.
| NUMBER OF SEQUENCES: 23
| CORRESPONDENCE ADDRESS: ADDRESSE: Baker & Botts, L.L.P. attn. Lisa Kole
| STREET: 30 Rockefeller Plaza
| CITY: New York
| STATE: New York
| STATE: New York
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                                                            1143 ACCCTCTCCTGTATGCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGTTTCC 1202
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                                                                                                     904 Accccarcarcrarecerrirercesesasasarricasaaacracererrasererrerrece 963
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AATATAAAGGACTCAAACGCGTGGAAAATATCTATCTTCTAAACTTGGCAGTTTCTAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER KEALABLE FUGDY disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/087,232A
FILING DATE: 28 MAY 1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 6/048,057
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
REGISTRATION NUMBER: 35,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-262
TELEPHONE: (212) 765-2519
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1376 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                     AAAAGCACATTGCCA 978
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COMPUTER READABLE FORM:
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, LOCATION: 240
US-09-087-232A-12
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                           AGGTTCAGGGAGCAGAGGTATAGCC
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APPLICANT: Dragic, Tatjana
APPLICANT: Olson, William
TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
FILE REPERENCE: 2048/610.10/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/796,202
CURRENT FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
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                             TCTATGTGCAAATGAGAAAAACACTA-
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Best Local Similarity 57.0%;
Matches 522; Conservative
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ORGANISM: human
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US-09-796-202-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
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Pred. No. 2.2e-62;
0; Mismatches 354;
                                                                                                                                                                                                                                                                       PA-0002
                                                                                                                                                            APPLICALL.

CLASSIFICATION:
ATJORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REPRENCE/DOCKET NUMBER: PA-00
TELECOMMUNICATION INFORMATION:
""" EDHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                    13.6%;
57.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid_
STRANDEDNESS: single
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CLONE: 91262810
US-09-016-434-1104
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Best Local Similarity
Matches 522; Conserv
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IMMEDIATE SOURCE
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Patent No. 6743594
GENERAL INFORMATION:
APPLICANT: Li, Yi
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Methods of Screening Using Human G-Protein
TITLE OF INVENTION: Chemokine Receptor HDGNR10 (CCR5)
FILE REFERENCE: 1488-1150005
CURRENT APPLICATION NUMBER: US/09/502,784A
                           GCTCTGCTGTGTTTGTGATCGGTGTCCTGGACAATCTCC
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Sequence 1, Application US/09502783A

Perent No. 6511826

GENERAL INFORMATION:

APPLICANT: Li, Yi

APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Polynuclectides Encoding Human G-Protein Chemokine Receptor TITLE OF INVENTION: HDGNR10

FILE REFERENCE: 1488: 1150006

CURRENT APPLICATION NUMBER: US/09/502,783A

CURRENT APPLICATION NUMBER: 08/466,343

PRIOR FILING DATE: 1995-06-06

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.0
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llarity 57.0%; Pred. No. 2.3e-62;
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APPLICANT: Ruben, Steven, M. Antibodies to Human G-Protein Chemokine Receptor HDGNR10 TITLE OF INVENTION: Antibodies to Human G-Protein Chemokine Receptor HDGNR10 TITLE OF INVENTION: (CRS Receptor) FILE REPERENCE: 1488.115003
CURRENT APPLICATION NUMBER: US/09/339,912A
CURRENT FILING DATE: 1999-06-1999.662
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR FILING DATE: 1998-11-18
PRIOR FILING DATE: 1998-06-06
NUMBER OF SEQ ID NOS: 99
SOFTWARE: Patentin version 3.0
              1142
                                                                                                                                                                                          1143 ACCCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGTTTCC 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 cogadecerioceaaaaareaaroraadecaaaredecaaceeeereeereeereeereereereereereereeree
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                                                     1076 ACAGGTIGGACCAAGCIATGCAGGTGACAGAGACTCTTGGGATGACGACTGCTGCATCA
                 1083 ACAATCTGGACAAAAGTGTTCACATCACTAAACTCATCGCCACCACCACTGCTGCATCA
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LOCATION: (259)..(1314)

OTHER INFORMATION: Description of Artifical Sequence: Genomic US-09-333-9128-1
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13.6%; Score 230.6; DB 4; Length 1
Best Local Similarity 57.0%; Pred. No. 2.3e-62;
Matches 522; Conservative 0; Mismatches 354; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/09339912A; Patent No. 6759519; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       1196 AAAAGCACATTGCCA 1210
                                                                                                                                                                                                                                                                                           1203 ATCTGCGTAGTAACA 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-09-339-912A-1
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Pred. No. 2.3e-62;
0; Mismatches 354; Indels
CURRENT FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 09/195,662
PRIOR PILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 06/466,343
PRIOR PILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VETSION 3.1
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Best Local Similarity 57.0%;
Matches 522; Conservative
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; OTHER INFORMATION:
US-09-502-784A-1
                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: RLi, Yi
APPLICANT: Ruben, Steven, M.
TITLE OF INVENDEN: Steven, M.
Human G-Protein Chemokine Receptor HDGNRIO (CCRS Receptor)
FILE REFERENCE: 1488.115002
CURRENT PPLICATION NUMBER: US/09/195,662A
CURRENT FILING DATE: 1998-11-18
PRIOR APPLICATION WINBER: 08466,343
PRIOR FILING DATE: 1995-06-06
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                             956 CTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACA 1015
                                                                                                                                                                                                                                                               TTGCATTTTTCCTGTCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCT 1082
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; NAME/KEY: CDS
; LOCATION: (259)..(1314)
; OTHER INFORMATION: Description of Artifical Sequence: Genomic
US-09-195-662A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence: Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09195662A Patent No. 6800729 GENERAL INFORMATION:
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US-09-195-662A-1
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1143 ACCTCTCTGTATGCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGTTTCC 1202
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                            ACTGCAAAAGGCTGAAGAGCATGACATCTACCTGCTCAACCTGGCCATCTCTGACC 487
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; Sequence 300, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                   June 18, 2005, 15:44:41; Search time 1070 Seconds (without alignments) 9850.853 Million cell updates/sec
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| cgn2_6/prodata/1/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/prodata/1/pubpna/PCT_MEW_PUB.seq:*
| cgn2_6/prodata/1/pubpna/NCT_MEW_PUB.seq:*
| cgn2_6/prodata/1/pubpna/USO6_NEW_PUB.seq:*
| cgn2_6/prodata/1/pubpna/USO6_NEW_PUB.seq:*
| cgn2_6/prodata/1/pubpna/USO8_NEW_PUB.seq:*
| cgn2_6/prodata/1/pubpna/USO8_NEW_NEW_Seq:*
| cgn2_6/prodata/1/pubpna/USO8_NEW_Seq:*
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| cgn2_6/prodata/1/pubpna/USO8_NEW_Seq:*
| cgn2_6/prodata/1/pubpna/USO8_NEW_NEW_Seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6054689 segs, 3103772919 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Result Query No. Score Match Length DB ID Description

1 1698 100.0 1698 19 US-10-717-597-300 Sequence 300, App 2 1693.6 99.7 1776 21 US-10-741-600-13 Sequence 15, Appl 4 1468.4 86.5 1475 15 US-10-223-088-15 Sequence 15, Appl 5 1468.4 86.5 1475 15 US-10-223-088-15 Sequence 15, Appl 6 1468.4 86.5 1475 15 US-10-223-089-15 Sequence 15, Appl 7 1468.4 86.5 1475 15 US-10-223-090-15 Sequence 15, Appl 7 1468.4 86.5 1475 15 US-10-223-090-15 Sequence 15, Appl 7 1468.4 86.5 1475 15 US-10-223-090-15

2222222	# # # # # # # # # # # # # # # # # # #	Sequence 11, Appl. Sequence 858, Appl. Sequence 857, Appl. Sequence 308, Appl. Sequence 22881, Appl. Sequence 22881, A Sequence 20554, A Sequence 20554, A Sequence 9067, Appl. Sequence 9067, Appl. Sequence 19, Appl. Sequence 21, Appl.
US-10-223-083-15 US-10-223-081-15 US-10-223-081-15 US-10-223-082-15 US-10-305-654-15	S US-10-225-567A-3 S US-09-967-76BA-31 1 US-10-843-641A-6 1 US-10-741-600-12 1 US-10-741-600-17 4 US-10-039-659-11 9 US-10-754-071-11 1 US-10-759-860-17 5 US-10-305-720-75 6 US-10-39-86-88-8 6 US-10-623-346-32	8 US-10-623-472 US-10-311-455 US-09-912-025- US-10-311-455 US-10-31-455 US-10-622-283 US-10-622-283 US-10-622-283 US-10-622-385 US-10-029-386 US-10-10-10-10-10-10-10-10-10-10-10-10-10-
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ALIGNMENTS

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APPLICANT: Twine, Natalie C.
APPLICANT: Trepicchio, William L.
APPLICANT: Trepicchio, William L.
APPLICANT: Slonim, Donna K.
APPLICANT: Slonim, Donna K.
APPLICANT: Slover, Jennifer A.
TITLE OF INVENTION NETHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
FILE REFERENCE: AM101000L
CURRENT APPLICATION NUMBER: US/10/717,597
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US 60/427,982
PRIOR PILING DATE: 2003-11-21
NUMBER OF SEQ ID NOS: 4904
SOFTWARE: Patentin version 3.2
NUMBER OF SEQ ID NOS: 4904
SOFTWARE: Patentin version 3.2
CURRENT Homo sapiens
US-10-717-597-300
Query Match
Best Local Similarity 100.0%; Prod. No. 0;
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61 TCCCTGAGCTCGGTGAGTGGGCCGCTAGAGCCACCAGGGGAATCAACAGTGGTTTCTCG 120	301 CATAGAAGGTGAACTGGAGAGCGATGAGCAATGTGACAAGTATGACGCCCAGGC 360	1 CTATCTTCTAAACTTGGGAGTTTCTTACTTTCTTGGTTACCCTGCCCTTCTGGGG 2 CTATCTTCTAAACTTGGAGTTTCTTGGTTTCTTGGTTACCCTGCCCTTCTGGGG 2 CTATCTTCTAAACTTGGAGTTTCTTGTTTTCTTGGTTACCCTGCCCTTCTGGGG 1 TCATGCTTGGGGGCGATCCCCATGTGTAAATTCTCATTGGACTGTACTTCGTGGGCCTGTA 1 TCATGCTGGGGGCGATCCCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTA 2 TCATGCTGRKGGCGATCCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTA 1 CAGTGAAACTAGAATTCTCATTGGACTGTAAATTCTCATTGGACTGTAATTCTTAAAATTCTCATTGGACTGTAAATTCTCATTGGACTGTAATTCTTAAAATTCTCATTGGACTTAAATTCTCAAAAAAAA	CAGIGAGACATTTTCAATTGCCTTCTGACAGAGGGCAGGGTTTTTGCACAA CAGTGAGACATTTTCAATTGCCTTCTGACTGTGCAAAGGTACCTAGTGTTTTTGCACAA GGGCAACTTTTTCTCAACAGGAGGAGGGGGTGCCCTGTGGCATTACAAGTGTTTTTGCACAA GGGCAACTTTTTCTCAGCCAGGAGGAGGGGGCCCTGTGGCATTACAAGTGTCCTGGC ATGGGTAACAGCCATTCTGGCCAGGAGGGTGCCTGTGGCATCATTACAAGTGTCCTGGC ATGGGTAACAGCCATTCTGGCCACTTTGCCTGAATACGTGGTTTATAAAACCTCAGATGGA ATGGGTAACAGCCATTCTGGCCACTTTGCCTGAATACGTGGTTTATAAAACCTCAGATGGA	AGACCAGAATACAAGTGTGCATTTAGCAGAACTCCTTCCT	972 TITIACATITCTCIATGTGCAAATGAGAAACACTAAGGTTCAGGGGGGGGGTATAG 1031 961 CCTITTCAAGCTTGTTTTTGCCATAATGGTAGTTCCTTCTTGATGTGGGCGCCCTACAA 1020 1032 CCTITTCAAGCTTGTTTTTGCCATAATGGTAGTTCTTCTTGATGTGGGGCGCCTACAA 1020 1021 TATTGCATTTTTCCTGCTCCACTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGA 1091 1092 TATTGCATTTTTCCTGCTCCACTTTCAAGAACACTTCTCCCTGAGTGACTGCAAGAGAG 1151 1091 CTACAATCTGGACAAAAGTGTTCAAAGAACACTTCTCCCTGAGTGACTGCACAGAGCAG 1151 1081 CTACAATCTGGACAAAAGTGTTCAACAAAACTCATCACCTGAGTGACTGCACTGCTGCAT 1140 1152 CTACAATCTGGACAAAAGTGTTCAACACTAAACTCATCGCCACCCCCCCTGCTGCAT 1211 1161 CAACCCTCCTGTATGCGTTTCTTGATGGGACATTTAGCAAATACCTCTCGCCGCTGTTT 1200
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CTGCCGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACA 1020
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                                                        CTGCCGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCCAGGGGGCAGTCTGCACA
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APPLICANT: Baker, Kevin P.
APPLICANT: Gerrara, Napoleone
APPLICANT: Gerraren, Mary E.
APPLICANT: Godward, Audrey
APPLICANT: Godward, Paul J.
APPLICANT: Godward, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Marsters, Scot A.
APPLICANT: Marsters, Scot A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Ye, Watanabe, Colin K.
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Publication No. US20030105011A1
GENERAL INFORMATION:
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Pred. No. 0;
0; Mismatches
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR PILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 383
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Best Local Similarity 99.9
Matches 1469; Conservative
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US-10-223-088-15
Sequence 15, Application US/1023308
Sequence 15, Application No. US20330105012A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Gerrara, Napoleone;
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
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         TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
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FILE OF INVENTION: TREATMENT OF DISORDERS FILE REFERENCE: P3235PLCS
CURRENT APPLICATION NUMBER: US/10/223,084
CURRENT FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-07-26
PRIOR PLING DATE: 2000-07-26
PRIOR PLING DATE: 2000-07-26
PRIOR PLING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR PRIOR APPLICATION NUMBER: PCT/US00/2010
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-24
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Best Local Similarity 99.9%;
Matches 1469; Conservative 0
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; ORGANISM: Homo sapiens
US-10-223-084-15
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                                                APPLICANT: Marsters, Scot A.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Poly Wood, William I.
APPLICANT: POLY COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235PLG
CURRENT APPLICATION NUMBER: US 10/081,056
PRIOR FILING DATE: 2000-06-23
PRIOR PELING DATE: 2000-06-23
PRIOR PELING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-08-27
PRIOR FILING DATE: 2000-08-27
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-23
PRIOR PELING DATE: 2000-08-23
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Pred. No. 0;
0; Mismatches
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Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 383
             Godowski, Paul J.
Gurney, Austin L.
Hillan, Kenneth J.
Marsters, Scot A.
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Best Local Similarity 99.9%;
Matches 1469; Conservative
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; ORGANISM: Homo sapiens
US-10-223-088-15
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                                                                                       1549 CGGAAATTTGTCTAAGATCACTTAACTAGGAAGTGGCAGAACTGATTCTCCAGCCCTGGT
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                                                                                                                                                                                                                                                                                               CGACATGAATAAATGTATTTAAAACATC 1698
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CURRENT APPLICATION NUMBER: US/10/223,087

CURRENT PAPLICATION NUMBER: US/10/223,087

CURRENT FILING DATE: 2002-02-20

PRIOR PILING DATE: 2002-02-20

PRIOR PLING DATE: 2000-06-23

PRIOR PLING DATE: 2000-06-23

PRIOR PLING DATE: 2000-07-20

PRIOR PLING DATE: 2000-07-20

PRIOR PLING DATE: 2000-07-25

PRIOR PLING DATE: 2000-07-26

PRIOR PLING DATE: 2000-07-26

PRIOR PLING DATE: 2000-08-23

PRIOR PLING DATE: 2000-08-17

PRIOR PLING DATE: 2000-09-15

PRIOR PLING DATE: 2000-09-16

PRIOR PLING DATE: 2000-09-18

PRIOR PRIOR PLING DATE: 2000-09-18

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APPLICATION NUMBER: PCT/US00/30952
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APPLICATION NUMBER: US 09/709,238
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Publication No. US20030109438A1
GENERAL INFORMATION:
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Stephan, Jean-Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferrara, Napoleone
Gerber, Hanspeter
Geriteen, Nary E.
Goddard, Audrey
Godwski, Paul J.
Gurney, Austin L.
Hillan, Kenneth J.
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Wood, William I.
Williams, P.Mickey
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Pred. No. 0;
0; Mismatches
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/USOO/32678
PRIOR FILING DATE: 2000-11-10
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/USOO/32678
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 2001-01-22
PRIOR FILING DATE: 2001-03-01
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Best Local Similarity 99.9
Matches 1469; Conservative
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469 CGTGGAAATATCTTCTAAACTTGGCAGTTTCTAACTTGTGTTTCTTGCTTACCCT 528	431 GTITITICACANGGOCAACTITITICACACAGAGGGGGGGCCCTGGCATCATTAC 108 421 GTITITICACAGGGGGAACTITICACACAGGGGGGGGGGG	1261 ACCACTTGTCCATAGTGGATAGGACTAGTCTCATTTCTCTGAGAAGAAACTAAGGCG 1320

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Qy 1369 Db 1141 Qy 1429 Db 1201 Qy 1549 Db 1321 Qy 1609 Db 1321 Qy 1609 Qy 1609 Qy 1609 Qy 1669	RESULT 9 US-10-223-089- Sequence 15, APPLICANT: AP	APPLICANT: TITLE OF INV. TITLE OF INV. TITLE OF INV. FILE REFERENCE CURRENT FILING PRIOR PLING PRIOR PRIOR PRIOR PLING PRIOR PLING PRIOR PRIOR PLING PRIOR P
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APPLICANT: Baker, Kevin P.
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APPLICANT: Gerrara, Napoleone
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey E.
APPLICANT: Goddard, Audrey E.
APPLICANT: Goddard, Audrey E.
APPLICANT: Goddard, Augrin L.
APPLICANT: Goddard, Augrin L.
APPLICANT: Marsers, Scot A.
APPLICANT: Marsers, Scot A.
APPLICANT: Marsers, Scot A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P.Mickey
APPLICANTON: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235PLC7
CURRENT FILING DATE: 2000-06-23
FRIOR APPLICATION NUMBER: US 60/213,637
PRIOR PILING DATE: 2000-07-26
PRIOR PILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR PILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/USOO/20110
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US-10-223-081-15
Sequence 15, Application US/10223081
Publication No. US20030186866A1
GENERAL INFORMATION:
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                                                                Length 1475;
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                                                               DB 15;
                                                             Score 1468.4;
Pred. No. 0;
0; Mismatches
                                                             86.5%;
                                                          Query Match
Best Local Similarity 99.9°
Matches 1469; Conservative
       TYPE: DNA
ORGANISM: Homo sapiens
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PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR PILING DATE: 2000-08-17
PRIOR PILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR PILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
Remaining Prior Application data removed - See Fill
NUMBER OF SEQ ID NOS: 383
LENGTH: 1475
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99.9%; Pred. No. 0;
ive 0; Mismatches
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Matches 1469; Conservative
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APPLICANT: Baker, Kevin P.
APPLICANT: Gerrara, Napoleone
APPLICANT: Gerriteen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godwaki, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Marsters, Scot A.
APPLICANT: Paul J.
APPLICANT: Paul J.
APPLICANT: Paul J.
APPLICANT: Paul J.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: William P. Mickey
APPLICANT: Ye, Wailam I.
APPLICANT: Ye, Wailam I. CGACATGAAATAAATGTATTTTAAAACATC 1698

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1081 GCAAGAATAAACATGGATTTTCATCTTTCTGCATTATTTCATGTAAATTTTCTACAC 1140
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US-10-305-654-15
Sequence 15, Application US/10305654
Publication No. US20030224984A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Befar, Napoleone
APPLICANT: Gerber, Hang-Peter
APPLICANT: Gerriteen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
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CURRENT FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: US 10/081,056

PRIOR FILING DATE: 2002-02-20

PRIOR PELING DATE: 2000-06-23

PRIOR PELING DATE: 2000-06-23

PRIOR PELING DATE: 2000-07-20

PRIOR PELING DATE: 2000-07-25

PRIOR PELING DATE: 2000-07-26

PRIOR PELING DATE: 2000-07-28

PRIOR PELING DATE: 2000-07-28

PRIOR PELING DATE: 2000-07-28

PRIOR PELING DATE: 2000-08-02

PRIOR PELING DATE: 2000-08-02

PRIOR PELING DATE: 2000-08-03

PRIOR PELING DATE: 2000-08-23

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PRIOR PELING DATE: 2000-08-24

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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.9%;
Matches 1469; Conservative 0
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; ORGANISM: Homo sapiens
US-10-223-082-15
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             GGCGCCCTACAATATTGCATTTTCCTGTCCACTTTCAAAGAACACTTCTCCCTGAGTGA
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APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gebrer, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwaki, Paul J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
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APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watlans, P.Mickey
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US-10-081-056-15
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APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Paoni, N. F.
APPLICANT: Paoni, J. F.
APPLICANT: Paoni, J. F.
APPLICANT: Stephan, J-P F.
APPLICANT: Watanabe, C.K.
APPLICANT: Watanabe, C.K.
APPLICANT: Williams, P.M.
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS FILE REFERENCE: P323SR1C1
CURRENT APPLICATION NUMBER: US/10/305,654
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 15
LENGTH: 1475
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Pred. No. 0;
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Best Local Similarity 99.9%;
Matches 1469; Conservative
                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homosapiens
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RECORD APPLICATION WINNESS. 185
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ö 1008 1009 GGGGCCCTACAATATTGCATTTTTCCTGTCCACTTTCAAAGAACACTTCTCCCTGAGTGA 1068 CGGTGTCCTGGACAATCTCCTGGTTGTGCTTATCCTGGTAAAATATAAAGGACTCAAACG 240 300 588 648 CGGTGTCCTGGACAATCTCCTGGTTGTGCTTATCCTGGTAAAATATAAAAGACTCAAACG 468 CGTGGAAAATATCTATCTTCTAAACTTGGCAGTTTCTAACTTGTGTTTCTTGCTTACCCT 528 708 480 768 9 999 948 TGACGCCCAGGCACTCTCAGCCCAGCTGGTGCCATCACTCTGCTCTGCTGTTTTGTGAT 408 481 AAGTGTCCTGGCATGGGTAACAGCCATTCTGGCCACTTTGCCTGAATACGTGGTTTATAA 540 1 GGAGCTCAGCCCAGTGGGCAGTCTGAAGATGGCCAATTACACGCTGGCACCAGAGGATGA 60 241 CGTGGAAAATATCTATCTACAACTTGGCAGTTTCTAACTTGGTTTCTTGCTTACCTT 289 ATATGATGTCCTCATAGAAGGTGAACTGGAGAGCGATGAGGCAGAGCAATGTGACAAGTA 301 GCCCTTCTGGGCTCATGCTGGGGGGGGATCCCATGTGTAAAATTCTCATTGGACTGTACTT CGTGGGCCTGTACAGTGAGACATTTTTCAATTGCCTTCTGACTGTGCAAAGGTACCTAGT AAGTGTCCTGGCATGGGTAACAGCCATTCTGGCCACTTTGCCTGAATACGTGGTTTATAA 601 TGATGAGACATTCTGGAAGCATTTTCTGACTTTTAAAATGAACATTTCGGTTCTTGTCCT CCCCCTATTTATTTTTACATTTCTTTATGTGCAAATGAGAAAAACACTAAGGTTCAGGGA GCCCTTCTGGGCTCATGCTGGGGGCGATCCCATGTAAAATTCTCATTGGACTGTACTT CGTGGGCCTGTACAGTGAGACATTTTTCAATTGCCTTCTGACTGTGCAAGGTACCTAGT GTTTTTGCACAAGGGCAACTTTTTCTCAGGAGGAGGAGGGTGCCCTGTGGCATCATTAC GTTTTTGCACAAGGGCAACTTTTTCTCAGCCAGGAGGGTGCCCTGTGGCATCATTAC 541 ACCTCAGATGGAAGACCAGAAATACAAGTGTGCATTTAGCAGAACTCCCTTCCTGCCAGC CCCCCTATTTATTTTACATTTCTCTATGTGCAAATGAGAAAAACACTAAGGTTCAGGGA **ACCTCAGATGGAAGACCAGAAATACAAGTGTGCATTTAGCAGAACTCCCTTCCTGCCAGC** Gapa DB 18; Length 1475; TGATGAGACATTCTGGAAGCATTTTCTGACTTTAAAAATGAACATTTCGGTTCT ö 229 GGAGCTCAGCCCAGTGGGCAGTCTGAAGATGGCCAATTACACGCTGGC 1; Indels Score 1468.4; Pred. No. 0; 0; Mismatches PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/USO1/17443
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
PRIOR PILING DATE: 2001-06-20
PRIOR PILING DATE: 2001-06-20
PRIOR PILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 15 86.5**%**; 99.9**%**; Best Local Similarity 99.9 Matches 1469; Conservative TYPE: DNA ORGANISM: Homosapiens Query Match Best Local Similarity LENGTH: 1475 US-10-081-056-15 409 181 61 589 349 469 529 361 421 709 883 661 649 969 829 949 셤 셤 셤 유 δ ò ò 요 ò g ò 셤 ò 셤 ઠે 셤 셤 용 ઠ ò ઠે ð 임 ð ઠે 셤

Matches 1457; Conservative 0; Mismatches 3; Indels 0; Gaps 239 CCAGTGGGCAGTCTGAAGATGGCCAATTACACGCTGGCACCAGGGATGAATATGATGTC 29 185 CCACAGGGCAGTCTGAAGATGGCCAATTACACGCTGGCACCAGGGATGAATATGATGTC 24 299 CTCATAGAAGGTGAACTGGAGAGCGATGAGGCAAGGATGAAGATATGATGATGTC 35 215 CTCATAGAAGGTGAACTGGAGAGCGATGAGGCAAGGAATGTGACAGTATGACGCCCAG 35 329 GCACTCTCAGCCCAGCTGGAGAGCGATGAGGCAATGTGACAGTATGACGCCCAG 36 359 GCACTCTCAGCCCAGCTGGTGCCATCACTCTGCTCTGCT	419 GACAATCTCCTGGTTGTTGTCTGGTAAAATTTAAGGACTCAAACGGGTGGAAAAT 47	8 4 7 7 8 8 9 9 4 8 9 7 9 7 9	605 AAGGCAACTTTTCTCAGCCAGAAGAGGTGCCCTGTGGCATTACAAGTGTCCTG 719 GCATGGGTAACAGCATTCTGGCCACTTTGCCTGAATACGTGGTTTATAAACCTCAGATG 665 GCATGGGTAACAGCCATTCTGGCCACTTTGCCTGAATACGTGGTTTATAAACCTCAGATG 665 GCATGGGTAACAGCCATTCTGGCCACTTTGCCTGAATACGTGGTTTATAAACCTCAGATG	779 GAAGACCAGAAATACAAGTGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACA	. 899 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	1019 AATATTGCATTTTTCCTGTCCACTTTCAAAGAACACTTCTCCCTGAGGTGACTGCAAGAGC 1	1139 ATCAACCCTCTCCTGTATGCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGT 119	y 1259 AggaAgaACCTGACCATTCCACCGAGTGTAAACTAGCATCCACCAAATGCAGGAGAA 1318
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ò	1559	1559 TCTAAGATCACTTAACTAGGAAGTGGCAGAACTGATTCTCCAGCCCTGGTAGCATTTGCT 1618	1618
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GenCore version 5.1.6
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- nucleic search, using sw model nucleic õ June 18, 2005, 06:34:54; Search time 666.776 Seconds (without alignments) 9615.040 Million cell updates/sec Run on:

US-10-623-472-32 1083

score: Title: Perfect

Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 seqs, 2959870667 residues

Searched:

8780412 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Beq Beq 08 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_16Dec04: geneseqn1980s:* Database

geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:* geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:*geneseqn2002as:* geneseqn2003as:* geneseqn2002bs:* geneseqn2003bs:* geneseqn1990s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs:

Description	Abb52033 Mouse CCR Ad030354 Mouse GPC Ad032911 Mus muscu Ad038349 Human SNP Ach89585 Human SNP Ach89585 Human GPN Ach89585 Human GPN Ach89585 Human RRO Ab195568 Human RRO Ad010304 Human sec Add11264 Human sec Add11264 Human sec Add31265 Human sec Add31265 Human sec Add31265 Human BC Ad037657 Human BC Ad037657 Human BC Ad037657 Human BC Ad03765 Human Che Ad03769 Human Che Ad05729 Human CCR
SUMMARIES	ABS52093 AD03034 AD03031 AD030319 AD038350 ACK89585 ABL88079 ADD10304 ADD11264 ADD11264 ADD11264 ADD1304 ADD41265 AD841265 AD841265 AD841265 AD841265 AD841265 AD841265 AD8413664
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Score	10 10 10 10 10 4 4 4 4 4 4 4 4 4 4 4 4 4
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ALIGNMENTS

BP. ABS52093 standard; cDNA; 1083 (first entry) Mouse CCR12 cDNA. 05-NOV-2002 ABS52093; ABS52093

Mouse; CCR12; gene; se; chemokine receptor; L-CCR; MCP-1; HEK cell; Monocyte Chemoattractant Protein-1; brain glial cell; ischaemia; asthma; inflammatory disease; degenerative brain disease; Alzheimer's disease; multiple sclerosis; neurodegenerative disease; neuroinflammatory disease; allergic encephalitis; chronic obstructive pulmonary disease; obstructive airway disease; neuroprotective; antiinflammatory

Мив вр.

WO200257779-A2.

25-JUL-2002.

18-JAN-2002; 2002WO-NL000039.

18-JAN-2001; 2001EP-00200181.

(UYGR-) RIJKSUNIV GRONINGEN.

ž Biber Boddeke EHWGM,

WPI; 2002-599725/64.

Identifying compounds for treating inflammatory or degenerative brain diseases, comprises testing the compound for its capacity to modulate or mimic Monocyte Chemoattractant Protein-1 binding with a chemokine receptor

Disclosure; Fig 8; 45pp; English.

The invention relates to identifying a candidate drug compound comprising testing the compound for its capacity to modulate or mimic Monocyte Chemoattractant Protein-1 (MCP-1) binding with a chemokine receptor

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capable of being expressed on brain glial cells and is known in the mouse as L-CKP or in humans as CRAM-B. The chemokine receptor expressed in a cultured cell comprising the cell transfected with a nucleic acid and a HEK cell, is useful in identifying a candidate drug compound for treating linflammatory or degenerative brain disease, e.g. ischaemta, Alzheimer's disease or multiple sclerosis. The agonist or antagonist is useful in the preparation of the pharmaceutical composition useful in treating enroded envelophalitis and chronic obstructive pulmonary diseases and obstructive airway diseases uch as allergic alrway diseases uch as allergic
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                                                                                                                                                                     G; 278
                                                                                                                                                                      Sequence 1083 BP; 237 A; 294 C; 274
                                                                                                                             airway diseases such as a
cDNA, also known as CCR12
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G protein-coupled receptor; GPCR; drug screening; diagnosis;

K transgenic mouse; neurological disorder; adrenal gland disorder;

K colon disorder; intestinal disorder; cardiovascular disorder;

M muscular disorder; blood disorder; immune disorder; bone disorder;

K idney disorder; liver disorder; immune disorder; cancer;

K idney disorder; liver disorder; prostate disorder; cancer;

K idney disorder; uterus disorder; prostate disorder; spleen disorder;

K why disorder; thyroid disorder; pancreas disorder; spleen disorder;

K thymus disorder; thyroid disorder; antiparkinsonian; antimanic;

K thymus disorder; thyroid disorder; antiparkinsonian; antimanic;

K thymus disorder; thyroid disorder; antidarkinsonian;

K thymus disorder; thyroid disorder; antidarkinceic; antidabetic;

K thymus disorder; antihiflammatory; vasotropic; antidacthoric; antidabetic;

K virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;

K immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
                                                                                                                              CCACGGTGCAATGATATCCCCTATCAAAGTAGTGGAGGCTATCAGCAAGCGCCTCCAAGG 1020
                                                                                                                                                                              1021 GAAGGTCATGGCAGGCCCATTGAACTGTACAGCAATTTGCATCAAAGGCAGGATATAATA 1080
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                                                             901 CCGCTGCTCTATTTGCTTCTTGACCGGAAGGCCTTTATGAGATACCTTCGCAGCCTGTTC 960
Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J,
Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse GPCR CMKBR1L2 polynucleotide, SEQ ID NO:1457.
                                                                                                                                                                                                                                                                                                                                                                   ВР
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Claim 151; SEQ ID NO 1457; 542pp; English

pectoris, Parkinson's disease.

The invention relates to human and mouse G protein-coupled receptors (GPCR8) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of erreating, preventing or disgnosing diseases of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic compounds useful in the treatment of GPCR-related diseases; a transgenic compounds useful in the treatment of GPCR-related diseases; a transgenic comparising a mutation in a different GPCR gene of the invention; and kits comprising substantion in a different GPCR gene of the invention in the comprising several mice, each of which has a mutation in a different GPCR gene of the invention. The invention further discloses variants of the GPCR polypetides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzhimier's disease, distributed, disease or schizophrenia); dispersation, diabetic neuropathy, Perkinson's disease or schizophrenia); dispersation, diabetic neuropathy, perkinson's disease or schizophrenia); crown's disease, diarrhoea, food poisoning or intratable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or more and joint disorders (e.g., obtocarthitis, rheumatoid arrhitis, and disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases). diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCK-encoding nucleic acid of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 1083 BP; 236 A; 295 C; 275 G; 277 T; 0 U; 0 Other;

ö CTGGACAACAGTGGGCCGGACCAAGTTCCGGCCCCCGAGTTCCTCCCCCCCAGCAGGTG 120 CTGGACAACAGTGGGCCGGACCAAGTTCCGGCCCCCGAGTTCCTCCCCCCCAGCAGGTG 120 180 ATCTTGGTGAAATACAAAGGACTCAAGAATCTGGGGAACATCTACTTCCTAAACCTGGCA 240 240 CTTTCAAACCTGTGTTTCCTGCTTCCCGTGCCGTTCTGGGCCCATACTGCAGACACGGGG 300 CTTTCAAACCTGTGTTTCCTGCTTCCCCTGCCGTTCTGGGCCCATACTGCAGCACACGGG 300 CGACTGGCCTCCATCTTCACGACAGTGTCTTGTGGTATTGTTGCGTGCATCCTGGCATGG 480 GCCATGGCTACTGCGCTCTCTTTGCCCGAGTCTGTTTTATGAGCCTCGGATGGAAGA 540 GAAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTCGGACTCCACTCCTCGGGCTTATAC 360 GAAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTCGGACTCCACTCCTCGGGCTTATAC 360 AGCGAGGIGTTTTCCAACATCCTCCTTGTGCAAGGATACAGGGTGTTTTCCCAAGGG 420 AGCGAGGTGTTTTCCAACATCCTCCTTGTGCAAGGATACAGGGTGTTTTCCCAAGGG 420 9 1 ATGGATAACTACACAGTGGCCCCGGACGATGAATATGATGTCCTAATCTTAGACGACTAC CTGCAGTTCTGCTGCGCGTGTTTGCGGTGTCTCTTGGACAACGTGCTGGCGGTGTTT crecaerrerecrecesererrecesresererresacaacaacagecrecesesrerr Arctrigateanaracanagacricaagaarcrigagaacarcrigitacriccranaccrigas Gaps 99.4%; Score 1076.6; DB 12; Length 1083; ö 4; Indels Pred. No. 0; 0; Mismatches 99.68; Best Local Similarity 99.6 Matches 1079; Conservative 241 361 61 181 181 481 Query Match 19 121 121 241 301 301 361 421 421 윱 g 8 8 ઠે g 8 6 8 6 6 र्व क्षे

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CTGCAGTTCTGCTGCGGGGGTGTTTGCGGTGGGTCTCTTGGACAACGTGCTGGCGGTGTTT CTGCAGTTCTGCTGCGGGTGTTTGCGGTGTCTTTGGACAACGTGCTGGCGGGGTTTT ATCTTGGTGAAATACAAAGGGCTCAAGAATCTGGGGAACATCTACTTCCTAAACCTGGCA ATCTTGGTGAAATACAAAGGACTCAAGAATCTGGGGAACATCTACTTCCTAAAACCTGGCA CITICAAACCIGIGITITCCIGCTICCCCTGCCGTICTGGGCCCATACTGCAGCACAGGG

121 565 625

181

685

301

241

CTGGACAACAGTGGGCCGGACCAAGTTCCGGCCCCCGAGTTCCTCTCCCCCCAGCAGGTG

180

624

564

300

744 360 804 420 864 480 924

GAAAGCCCTGGCAACGCGACCTGTAAAGTTCTTGTCGGACTCCACTCCGGGCTTATAC 745 GAAAGCCCTGGCAACGGGACCTGTAAAGTTCTTGTCGGACTCCACTCCTCGGGCTTATAC 361 AGCGAGGTGTTTTCCAACATCCTCCTCCTTGTGCAAGGATACAGGGTGTTTTCCCAAGGG AGCGAGGTGTTTTCCAACATCCTCCTTGTGCAAGGATACAGGGTTTTCCCAAGGG

805

421

865

481

CGACTGGCCTCCATCTTCACGACAGTGTCTTGTGGTATTGTTGCGTGCATCCTGGCATGG GCCATGCCTACTGCGCTCTCTTTGCCCCGAGTCTGTGTTTTATGAGCCTCGGATGGAAAGA

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Novel non-human transgenic animal, especially transgenic mice useful for identifying an agent that modulates expression or function of target gene, comprises disruptions in target G protein-coupled receptor gene.
/note= "Sequence flanking Neo insert in targetting
construct"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 15; 101pp; English.
                                                                                                                  10-JUL-2000; 2000US-0217253F.
10-JUL-2000; 2000US-0217255F.
10-JUL-2000; 2000US-0217255F.
11-JUL-2000; 2000US-0217357F.
11-JUL-2000; 2000US-0217347F.
11-JUL-2000; 2000US-0217347F.
12-JUL-2000; 2000US-021837F.
12-JUL-2000; 2000US-021837F.
12-JUL-2000; 2000US-021837F.
12-JUL-2000; 2000US-021837F.
12-JUL-2000; 2000US-021837F.
12-JUL-2000; 2000US-021837F.
12-JUL-2000; 2000US-022183F.
12-JUL-2000; 2000US-022183F.
12-JUL-2000; 2000US-022183F.
12-JUL-2000; 2000US-022183F.
12-JUL-2000; 2000US-022183F.
15-NOV-2000; 2000US-024940RF.
16-JAN-2001; 2001US-026213F.
                                                                     10-JUL-2001; 2001WO-US021923
                                                                                                                                                                                                                                                                                                                                         Brennan TJ;
                                                                                                                                                                                                                                                                                                                    (DELT-) DELTAGEN INC
                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-164574/21.
P-PSDB; AAE20602.
                               40200203793-A2
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1044

601 AAGTACGTTCTGACGTCAAAATGATCATCTTGGTACTTGCTTTTCCTCTGCTGGTTTTT

925 GCCATGGCTACTGGGCCTCTTTGGCCCGAGTCTGTTTTATGAGCCTCGGATGGAAAGA

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984 600

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The invention relates to a non-human transgenic animal having targetted G -protein coupled receptor (GPCR) gene disruptions in melanocortin-3 gene -protein coupled receptor 9A gene, glucocorticoid induced receptor Gene, orphan GPR15 gene, orphan GPR14 gene, orphan GPR15 gene, creansgenic animal is useful for identifying an agent that medulates the transgenic animal is useful for identifying an agent that medulates the expression or function of the target gene, for identifying an agent that amountains on succession or function of the target gene, for identifying an agent that amountains or function of the target gene, for identifying an agent that amountains or construct is useful for producing a transgenic animal.

The transgenic construct is useful for producing a transgenic animal, the farget gene. The transgenic animal is useful for profucing a transgenic animal is useful for profucing a transgenic animal is useful for diseases, such as neurological, neuropsychological or psychotic illnesses. The transgenic animal is also useful as models for diseases, disorders or conditions associated with phenotypes relating to a disruption in a target, and to identify pharmaceuticals, therapies, conditions which may be effective in treating a disease or the expression of the target gene is useful as a therapeutic for treating the conditions associated with a disruption of the target gene is useful as a therapeutic for treating conditions associated with a disruption of the target gene is useful as the target gene. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence is mouse GPCR beta chemokine receptor (E01) gene
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ô Gaps Length 2045; ô 4; Indels DB 6; 0; Mismatches Score 1076.6; Pred. No. 0; 99.4%; Matches 1079; Conservative Local Similarity Query Match

Seguence 2045 BP; 492 A; 509 C; 491 G; 553 T; 0 U; 0 Other;

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65.2%; Pred. No.

Best Local Similarity

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1525 TAA 1527

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Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                     Myocardial infarction; detection; single nucleotide polymorphism; SNP;
cardiant; gene therapy; human; gene; ds.
                                                                   Human SNP containing myocardial infarction-associated gene, SEQ ID 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13; Length 1646;
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                                                                                                                                                                                                                                                                                                                                Claim 7; SEQ ID NO 12; 145pp; English.
                                                                                                                                                                                                                                                  Iakoubova 0;
                 ВР
                ADQ38349 Btandard; DNA; 1646
                                                                                                                                                                                    20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-046612P.
23-SEP-2003; 2003US-0504955P.
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P-PSDB; ADQ39177.
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has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises an isolated nucleic acid molecule comprising at least comprises an isolated nucleic acid molecule comprising at least the specification or its complement and encoding any one of the amino the specification or its complement and encoding any one of the amino can acid esquence given in the specification; an antibody that specification and which as pecification; an isolated polypeptide comprising an SNP given in the specification and which is between the containing an SNP given in the engeth; a kit for detecting an SNP in a nucleic acid molecule, a buffer and an enzyme; a method of detecting an SNP given in the engeth of a cidencial infarction and an enzyme; a method of detecting an SNP given in the myocardial infarction. The novel detecting a variant polypeptide; and myocardial infarction and increased or detecting a method is useful in identifying an agent useful in treating or preventing an enthod is useful in identifying myocardial infarction and for preparing a method is useful in identifying myocardial infarction and for preparing a method is useful in identifying an approximation and for preparing a method is useful in identifying myocardial infarction and propagating and processed in the invention may be used in gene therapy. The method is useful in identifying myocardial infarction and for preparing a method is useful in identifying myocardial infarction and processed or processed in the processed in the processed or processed in the processed or proc
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The invention relates to a novel method for identifying an individual who
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          electronic sequence listing downloaded from the WIPO website.
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The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least a contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequence given in the specification; an antibody that specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polymucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting an SNP in a method for identifying an agent useful in treating or preventing and an enthod for identifying an agent useful in treating or preventing.
   1198 ACATCGAGGGAAGAACCTGACCATTCCACGGAAGTGTAAACTAGCATCCACCAAATGCAA 1257
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                                                                                                                                          DB 13; Length 1776;
                                                                                                                                                                                                                                      33;
                                         Sequence 1776 BP; 456 A; 425 C; 412 G; 472 T; 0 U; 11 Other;
                                                                                                                                                                                        Pred. No. 6.1e-117;
5; Mismatches 338;
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Pred. No. 6.1
                                                                                                                                          39.1%;
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide expression, comprising any of the 27,400 fully defined nucleotide according at least 8 amino acids of any of the 6888 amino acid sequences concing at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that thyridates under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human cells or the plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon addressably isolatable or amplifiable from the plurality), a single con addressably isolatable or amplifiable from the plurality), a single con according human gene expression, a wector comprising at least 8 contiguous amino acids of any of the above- mentioned amino acid sequences (optionally with conservative amino acid aubstitutions), an isolated antibody that binds specifically to a peptide cited above, and/or licensing single exon probes or methods of solating and/or licensing single exon probes or methods and expression a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records cated above. The probes may be used as tools for surveying expression analysis. The probes may be used as tools for surveying
1264 GGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCAGGGGGCAGTCTGCACAAGGC 1323
                                       CCTCCAAGGGAAGGTCATGGCGCCCATTGAACTGTACAGCAATTTGCATCAAAGGCAG 1071
                                                                            1324 acarceaggaagaaccreaccarrecacceaagreraaacragcarecaccaarecaa 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human genome-derived single exon nuclaic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; probe; 88; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                             Human genome derived Bingle exon probe #22780.
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                                                                                                                                                                                                                                                                  ACH89585 standard; DNA; 1140 BP.
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(HANZ/) HANZEL D K.
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tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising smaller genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded paptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
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                                                                                                                                                                                                                                  Query Match 39.0%; Score 422; DB 12; Length 1140; Best Local Similarity 65.5%; Pred. No. 1.1e-116; Matches 709; Conservative 0; Mismatches 340; Indels 33;
                                                                                                                                                                                                    Sequence 1140 BP; 294 A; 275 C; 241 G; 330 T; 0 U; 0 Other;
                                                                                                                                                                   seqdata.uspto.gov/sequence.html?DocID=20030194704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CTGGACAACAGTGGGCCGGACCAAGTT-----CCGGCCCCCGAGTTCCTCCCCCAG
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39.0%; Score 422; DB 6; Length 1475;
Best Local Similarity 65.5%; Pred. No. 1.3e-116;
Matches 709; Conservative 0; Mismatches 340; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
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Godowski P
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                                                                                                                                                                                                                                         CGCTGTTTCCATCTGCGTAGTAACACCCCCACTTCAACCCAGGGGGCAGTCTGCACAAGGC 1008
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                                                                                                                                                                                                                                                                                                                    ACATCGAGGGAAGAACCTGACCATTCCACCGAAGTGTAAACTAGCATCCACCAAATGCAA 1068
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                                                                                                                                                     TGCATCAACCCTCTCTGTATGCGTTTCTTGATGGGA---CATTTAGCAAATACCTCTGC 948
                     891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; angiogenesis, cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiatteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; theumacoid arthritis; myocardial infarction; thromopophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
                                                          AGCAGCTACAATCTGGACAAAGTGTTCACATCACTAAACTCATCGCCACCACCACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO1873 cDNA sequence SEQ ID NO:15.
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18-SEP-2000; 2000US-0220978P.
18-SEP-2000; 2000US-02664510.
24-OCT-2000; 2000US-0242922P.
08-NOV-2000; 2000US-0263938.
01-NOV-2000; 2000WO-US030952.
10-NOV-2000; 2000WO-US030873.
01-DEC-2000; 2000WS-03747259.
20-DEC-2000; 2000WS-03747259.
22-JAN-2001; 2001US-0076699.
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2000WO-US023328.
2000US-0230978P.
2000US-00664610.
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2001WO-US006520.
2001WO-US006666.
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01-MAR-2001; 2001WO-US006666.
09-MAR-2001; 2001US-00802706.
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2000US-0219556P.
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25-JUL-2000;
28-JUL-2000;
02-AUG-2000;
17-AUG-2000;
23-AUG-2000;
24-AUG-2000;
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ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polymucleotides have cardiant, cytostatic, antianglogenic, hypotensive, vulnerary and antiarteriosclarotic activities, and can be used in gene therapy. The PRO polymucleotides, proteins, agonists and antegonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paoni NF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               One hundred and eighty seven nucleic acids encoding PRO polypeptides. useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ferrara N, Gerber H, Gerritsen ME, Goddard A; PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, FF, Watanabe CK, Williams PM, Wood WI, Ye W;
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14-MAR-2001; 2001US-00808689.
22-MAR-2001; 2001US-00816744.
05-APR-2001; 2001US-00818366.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854280.
25-MAY-2001; 2001US-00866028.
25-MAY-2001; 2001WS-0086034.
25-MAY-2001; 2001WS-00870574.
30-MAY-2001; 2001WS-US017092.
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2000US-006451369.
2000US-006651360.
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2000US-00747259.
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2001US-0076666.
2001US-00808689.
2001US-008081366.
2001US-00854289.
2001US-00854289.
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2001US-00866034.
      2001WO-US021735
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20-JUN-2001; 2001WO-US019692
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
PAN J.
PANNI N P.
STEPHAN J F.
WATLANABE C K.
WILLIAMS P M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GERBER H.
GERRITSEN M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENENTECH INC.
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FERRARA N.
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10-MAY-2001; 2
25-MAY-2001; 2
25-MAY-2001; 2
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25-JUL-2000;
02-JUL-2000;
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28-FEB-2001;
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22-MAR-2001;
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30-MAY-2001;
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Godowski P
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(BAKE/)
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(GODD/)
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      952 AGCCTGTTCCCACGGTGCAATGATATCCCCTATCAAAGTAGTGGAGGCTATCAGCAAGCG 1011
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368 CTGTACAGTGAGACATTTTTCAATTGCCTTCTGACTGTGCAAAGGTACCTAGTGTTTTTG 427
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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovasecular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal. Paoni NF rber H, Gerritaen ME, Goddard A; Hillan KJ, Marsters SA, Pan J, Williams PM, Wood WI, Ye W; Gerber H, Claim 1; Fig 15; 567pp; English. PJ, Gurney AL, JF, Watanabe CK, P-PSDB; ABB95430

Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antianglogenic; hypotensive; vulnerary; antiateriosclerotic; gene; se

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angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumous angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention
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                                                                                                                                                                      Score 422; DB 6; Length 1475;
Pred. No. 1.3e-116;
0; Mismatches 340; Indels 33;
                                                                                                                     Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
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Best Local Similarity 65.5%;
Matches 709; Conservative
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952 AGCCTGTTCCCACGGTGCAATGATATCCCCTATCAAAGTAGTGGAGGCTATCAGCAAGCG 1011
                                                                        965 cecrerriccarcreceraeraeracececacricaacecaasesesesererecadades 1024
                                                                                                                                                                                                                                    1025 ACATCGAGGGAAGAACCTGACCATTCCACGAAGTGTAAACTAGCATCCACCAAATGCA 1084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid encoding a secreted and transmembrane polypeptide for treating a cardiovascular, endothelial, or angiogenic disorder in a mammal, such as cancer or age-related macular degeneration.
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myocardial infarction; cardiac hypertrophy; trauma; cancer;
age-related macular degeneration; angiogenesis;
endothelial cell apoptosis; smooth muscle cell growth;
endothelial cell tube formation.
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A, Pan J,
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J, Hillan KJ, Marsters SA,
PM, Wood WI, Ye W;
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20-JUN-2001; 2001WO-US019592.
09-JUL-2001; 2001WO-US021735.
20-FEB-2002; 2002US-00081056.
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Godowski PJ, Gurney AL, H
Watanabe CK, Williams PM,
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952 AGCCTGTTCCCACGGTGCAATGATATCCCCTATCAAAGTAGTGGAGGCTATCAGCAAGCG 1011
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L, Hillan F
PM, Wood
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09-JUL-2001; 2001WO-US021735.
20-FEB-2002; 2002US-00081056.
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Godowski PJ, Gurney AL, Hi
Watanabe CK, Williams PM,
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P-PSDB; ADD11265.
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cell tube formation. The present sequence represents a cDNA encoding PRO polypeptide of the invention.
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    39.0%; Score 422; DB 10; Length 1475;
al Similarity 65.5%; Pred. No. 1.30-116;
709; Conservative 0; Mismatches 340; Indels 33;
                                                       Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
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The invention relates to an isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded by the nucleic acid, or an agonist or antegonist, is used to treat a cardiacular, endotholial, or anglogenic disorder in a mammal, or has cardiac hypertrophy, trauma, a cancer, or age-related macular degeneration. The cardiac hypertrophy is characterised by the presence of an elevated level of PGF-2 alpha. A PRO polypeptide, given in the specification, or an agonist is used to inhibit or stimulate endothelial call growth in a mammal. PRO149 is used to inhibit or alimilate endothelial chypertrophy. PRO136 or PRO149 is used to stimulate angiogenesis.

PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO polypeptide, given in the specification, or an agonist is used to induce endothelial cell tube formation. The present sequence represents a cDNA encoding a
965 CGCTGTTTCCATCTGCGTAGTAACACCCCCACTTCAACCCCAGGGGCAGTCTGCACAAGGC 1024
                                                                                                                                                                                       1025 ACATCGAGGGAAGAACTGACATTCCACCGAAGTGTAAACTAGCATCCACCAAATGCAA 1084
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                                                                                                                               CCTCCAAGGGAAGGTCATGGCAGGCCCATTGAACTGTACAGCAATTTGCATCAAAGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ss; gene; human; secreted protein; transmembrane protein; cardiovascular disorder; endothelial disorder; anglogenic disorder; myocardial infarction; cardiac hypertrophy; trauma; cancer; age-related macular degeneration; anglogenesis; endothelial cell apoptosis; smooth muscle cell growth; endothelial cell tube formation.
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(J, Marsters SA,
II, Ye W;
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The invention relates to an isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded by the nucleic acid, or an agonist or antagonist, is used to treat a cardiovascular, endothelial, or angiogenic disorder in a mammal, cardiovascular, endothelial, or angiogenic disorder in a mammal, cardioratrophy, trauma, a cancer, or age-related macular or has cardiac hypertrophy, trauma, a cancer, or age-related macular degeneration. The cardiac hypertrophy properties by the presence of an elevated level of PGF-2 alpha. A PRO polypeptide, given in the specification, or an agonist is used to inhibit or stimulate endothelial chypertrophy. PRO1376 or PRO1449 is used to simulate angiogenesis. Chypertrophy. PRO1376 or PRO1449 is used to simulate angiogenesis. PRO4302 or an agonist is used to induce endothelial call under or inhibit smooth muscle cell growth, or to induce endothelial cell tube formation. The present sequence represents a cDNA encoding a PRO polypeptide of the invention.
965 CGCTGTTTCCATCTGCGTAGTAACACCCCACTTCAACCCCAGGGGGCAGTCTGCACAAGGC 1024
                                                                                             1025 ACATCGÁGGGÁAGAACCTGACCATTCCACGÁAGTGTAAACTAGCATCCACCAAATGCAA 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acids encoding a secreted and transmembrane polypeptide for treating a cardiovascular, endothelial, or angiogenic disorder in a mammal, such as cancer or age-related macular degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stephan JF;
                                                         1012 CCTCCAAGGGAAGGTCATGGCAGGCCCATTGAACTGTACAGGCAATTTGCATCAAAGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                       disorder;
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myocardial infarction; cardiac hypertrophy; trauma; cancer,
age-related macular degeneration; anglogenesis;
endothelial cell apoptosis; smooth muscle cell growth;
endothelial cell tube formation.
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KJ, Marsters SA,
WI, Ye W;
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Wood WI,
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2001WO-US021735.
2002US-00081056.
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Watanabe CK, Williams PM,
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P-PSDB; ADD37058.
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09-JUL-2001;
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                                                                                                                 Gapa
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                                                                             Length 1475;
                                       Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
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                                                                         . Match 39.0%; Score 422; DB 10; Local Similarity 65.5%; Pred. No. 1.3e-116; les 709; Conservative 0; Mismatches 340;
   of the invention.
 PRO polypeptide
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09-JUL-2001; 2001WO-US021735.
20-FEB-2002; 2002US-00081056.
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                     Length 1475;
Sequence 1475 BP; 399 A; 351 C; 317 G; 408 T; 0 U; 0 Other;
                   Query Match 39.0%; Score 422; DB 10; Length 1. Best Local Similarity 65.5%; Pred. No. 1.3e-116; Matches 709; Conservative 0; Mismatches 340; Indels
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myocardial infarction; cardiac hypertrophy; trauma; cancer;
age-related macular degeneration; anglogenesis;
endothelial cell apoptosis; smooth muscle cell growth;
endothelial cell tube formation.
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Stephan JF; Goddard A; Pan J, Baker KP, Ferrara N, Gerber H, Gerritsen ME, Gov Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Watanabe CK, Williams PM, Wood WI, Ye W;

P-PSDB; ADE41266.

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO205 or PRO214, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and for treating disorders involving

Claim 2; SEQ ID NO 15; 492pp; English.

The invention relates to an isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded by the nucleic acid, or an agonist or antagonist, is used to treat a cardiovascular, endothelial, or angiogenic disorder in a mammal, preferably a human. The human may have suffered a myocardial infarction or has cardiac hypertrophy, trauma, a cancer, or age-related macular degeneration. The cardiac hypertrophy is characterised by the presence of an elevated level of PGF-2 alpha. A PRO polypeptide, given in the specification, or an agonist is used to inhibit or stimulate endothelial call growth in a mammal. PRO31 or an agonist is used to inhibit cardiac. Hypertrophy. PRO3376 or PRO349 is used to stimulate angiogenesis. PRO4302 or an agonist is used to induce endothelial call apoptosis. A PRO polypeptide, given in the specification, or an agonist is used to induce endothelial call tube formation. The present sequence represents a cDNA encoding a call tube formation. The present sequence represents a cDNA encoding a control or an agonist of the invention.

Tue Jun

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Human PRO polynucleotide #8.
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Stephan JF, Watanabe CK,
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The invention relates to human PRO polypeptides and the PRO polymucleotides encoding them. The invention also relates to treating cardiovascular, endothelial or angiogenic disorders in mammals, inhibiting endothelial or angiogenic disorders in mammals, inhibiting endothelial or all growth, stimulating endothelial cell growth, stimulating endothelial cell growth, stimulating endothelial cell growth, stimulating endothelial cell growth, stimulating angiogenesis or smooth muscle cell growth by administering polypeptides of the invention. The PRO polypeptides and polynucleotides are useful for treating cardiovascular, endothelial or angiogenic disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma, cancer or age-related macular degeneration, rand for polynucleotides are useful as hybridisation probes in chromosome and gene mapping and in generating antisense RNA and DNA, and for chromosome identification and tiseue typing. The PRO polypeptides and polynucleotides are also useful in gene therapy and as molecular weight markers for protein in gene therapy and as molecular weight markers for protein
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KJ, Marsters SA, Pan J,
ns PM, Wood WI, Ye W;
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Human; PRO; gene; se; cardiovascular disorder; endothelial disorder; angiogenic disorder; endothelial cell growth; cardiac hypertrophy; cell apoptosis; cell tube formation; angiogenesis; semooth muscle cell growth; myocardial infarction; trauma; cancer; age-related macular degeneration; cytostatic; cardiant; cerebroprotective; ophthalmological; vulnerary.
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99US-00403297.
99US-00423741.
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                                     ATGGATAACTACACAGTGGCCCCGGACGATGAATATGATGTCCTAATCTTAGACGACTAC
                                                               CTGGACAACAGTGGGCCGGACCAAGTT-----CCGGCCCCCGGAGTTCCTCCCCCCAG
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The invention relates to human PRO polypeptides and the PRO polymorlectides encoding them. The invention also relates to treating polymorlectides encoding them. The invention also relates to treating cardiovascular, endothelial or angiogenic disorders in mammals, inhibiting endothelial cell growth, stimulating endothelial cell growth, stimulating angiogenesis or smooth muscle cell growth by administering polypeptides angiogenesis or smooth muscle cell growth by administering polypeptides of the invention. The PRO polympthides and polymuclectides are useful for treating cardiovascular, endothelial or angiogenic disorders, e.g. mycoradial infarction, cardiac hypertrophy, trauma, cancer or age-related macular degeneration. The PRO polymuclectides are useful as hybridisation probes in chromosome and gene mapping and in geneting antisense RNA and DNA, and for chromosome identification and tissue typing. The PRO polymptides and polymuclectides are also useful in gene therapy and as molecular weight markers for protein clear therapy and as molecular weight markers for protein polymuclectide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at
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New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or PRO21383, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.
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                                                                                                                   Claim 2; SEQ ID NO 15; 494pp; English
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,, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PM, Wood WI, Ye W;
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10-NOV-2000; 2000WG-US032678

28-FEB-2001; 2001WG-US036665

01-MAR-2001; 2001WG-US006665

01-MAR-2001; 2001WG-US006666

02-MAY-2001; 2001WG-US036669

05-APR-2001; 2001WG-US0366634

25-MAY-2001; 2001WG-US017092

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Watanabe CK, Williams PM,
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New isolated antigenic peptides e.g., for G protein-coupled receptors
The present for diagnosing and designing drugs for treating conditions
In which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
AX
The present invention describes antigenic peptides (1) comprising (a)
By Disclosure, Pig 1; 523pp; English.

The present invention describes antigenic peptides (1) comprising (a)
CCC any one of 1601 sequences (see ABP22019 to ABP83619) of 12-24 amino
CCC any one of 1601 sequences (see ABP22019 to ABP83619) of 12-24 amino
CCC and (2) an isolated antibody having high specificity and high affinity or
CCC and (2) an isolated antibody having high specificity and high affinity or
CCC and (2) an isolated antibody specifies for GPCRs are useful for detecting an
CCC antibody against a particular GPCR, (1) can be used as GPCR modulators and in
CCC antibody against a particular GPCRs, and in the production of specific
CCC antibody against a particular GPCRs, and in the production of specific
CCC presence or absence of corresponding GPCRs. The antipodies for
CCC GPCRs and antibodies are useful for diagnosing and designing drugs for
CCC GPCRs and antibodies are useful for diagnosing and designing drugs for
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CCC GPCRs and antibodies are useful for diagnosing and designing drugs for
CCC GPCRs and antibodies are useful for diagnosing and designing drugs for
CCC GPCRs and antibodies are useful for diagnosing and designing drugs for
CCC GPCRs and antibodies are useful for diagnosing and designing drugs for
CCC GPCRs and antibodies are useful for diagnosing and designing drugs for
CCC GPCRs and antibodies are useful for disease, antibodies are
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39.0%; Score 422; DB 8; I
Best Local Similarity 65.5%; Pred. No. 1.3e-116;
Matches 709; Conservative 0; Mismatches 340; 61 260 115 320 175 380 235 295 495 415

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11 ABD20648	11 ABD20815	3 AAA34983	3 AAA35150	3 AAF21272	3 AAP21105	6 ABL68124	6 ABT11034	10 ABZ96966	10 ABZ96799	3 AAA35151	11 ABD20816	3 AAP21273	10 AB296967	12 AD030063	10 ACA56158	12 ADIS5954	2 AAT99543	11 ADP03560	2 AAV04641	6 AAS17436	6 AAD42836	6 ABL32885	6 ABL32884	5 AAF93267
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ALIGNMENTS

ABS52092 standard; cDNA; 1035 BP.

RESULT 1

(first entry)

05-NOV-2002 ABS52092;

Human; CCR12; gene; 88; chemokine receptor; CRAM-B; MCP-1; HEK cell; Monocyte Chemoattractant Proteán-1; brain glial cell; ischaemia; asthma; inflammatory disease; degenerative brain disease; Alzheimer's disease; multiple aclerosis; neurodegenerative disease; neuroinflammatory disease; allergic encephalitis; chronic obstructive pulmonary disease; obstructive airway disease; neuroprotective; antinflammatory. identifying compounds for treating inflammatory or degenerative brain 18-JAN-2002; 2002WO-NL000039. 18-JAN-2001; 2001EP-00200181. (UYGR-) RIJKSUNIV GRONINGEN. Biber K; WPI; 2002-599725/64. Human CCR12 cDNA. Boddeke EHWGM, WO200257779-A2 Homo sapiens. 25-JUL-2002.

The invention relates to identifying a candidate drug compound comprising testing the compound for its capacity to modulate or mimic Monocyte Chemoattractant Protein-1 (MCP-1) binding with a chemokine receptor Disclosure, Fig 8; 45pp; English.

diseases, comprises testing the compound for its capacity to modulate or mimic Monocyte Chemoattractant Protein-1 binding with a chemokine

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capable of being expressed on brain glial cells and is known in the mouse as L-CCR or in humans as CRAM-B. The chemokine receptor expressed in a cultured cell comprising the cell transfected with a nucleic acid and a HEK cell, is useful in identifying a candidate drug compound for treating inflammatory or degenerative brain disease, e.g. ischaemia, Alzheimer's disease or multiple sclerosis. The agonist or antagonist is useful in the preparation of the pharmaceutical composition useful in treating neurodegenerative and neuroinflammatory diseases such as allergic encephalitis and chronic observative pulmonary disease and obstructive anixary diseases such as allergic encephalitis and chronic observative pulmonary disease and obstructive anixary diseases.
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100.0%; Pred. No. 0;
tive 0; Mismatches
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Best Local Similarity 100.
Matches 1035; Conservative
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TCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGAGCAGCTACAATCTGGACAAA

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dendritic cell, macrophage, inflammation, asthma; 98.
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                 841 AGIGITCACATCACTAAACTCATCGCCACCCACCCACCCAGCTGCATCAACCCTCTCCTGTAT
                                                      GCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGTTTCCATCTGCGTAGTAAC
                                                                     901 GCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGTTTCCATCTGCGGTAGTAAC
                                                                                                                            AGTGTTCACATCACTCATCGCCACCACCACTGCTGCATCAACCCTCTCTGTAT
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                                                                                                                                                                                                                                                                                                                                            Human macrophage/dendritic cell chemokine receptor encoding cDNA
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49. .1119
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/product= "M/DC
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96US-0028329P.
97US-0048593P.
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P-PSDB; AAW48087.
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11-OCT-1996;
04-JUN-1997;
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Human, gene, 88; thymus expressed chemokine; TECK; chemokine; MIP-3alpha; MIP-3beta; dendritic cell receptor for chemokine; DC CR; M/DC CR; asthma; monocyte/dendritic cell receptor for chemokine; inflammatory condition; abnormal physiclogy; abnormal proliferation; degeneration; atrophy; antiasthmatic; cytostatic.
                                                                                                                                                                                                                                  Human monocyte/dendritic cell receptor for chemokine (M/DC CR) cDNA
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96US-0028329P.
97US-0048593P.
97US-00887977.
                  1105 TCCACCGAAGTGTAA 1119
                                                                                                                 standard; cDNA; 1547
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Matches 1035; Conservative
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P-PSDB; ABU09081.
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                                                                            RESULT 3
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                                                                                                ATGCCCAATTACACGCTGGCACCAGGGGTGAATATGATGTCCTCATAGAAGGTGAACTG 144
                                                                                                                                                    GAGAGCGATGAGGCAGGCAATGTGACAAGTATGACGCCCAGGCACTCTCAGCCCAGCTG 120
                                                                                                                                                                                                                                  GTGCCATCACTCTGCTCTGTGTGTTTGTGATCGGTGTCCTGGACAATCTCCCTGGTTGTG 180
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The invention relates to nucleic acids encoding the chemokines TECK, MIP-3alpha, MIP-3beta, DC CR and M/DC CR. The polypeptide sequences are useful in isolating DNA clones encoding the chemokines, for generating antibodies, and for predicting oligomucleotides for screening a library to isolate species variants. A nucleic acid encoding a chemokine polypeptide can be used to identify genes, mRNA and cDNA species which encode related or homologous ligands, as well as DNA encoding homologous proteins from different species. The chemokines and antibodies which to the polypeptides are useful in the treatment of conditions associated with abnormal physiclogy or development, including inflammatory conditions such as asthma, abnormal polification, regeneration, degeneration and atrophy. This sequence represents cDNA encoding the human monocyte/dendritic cell receptor for chemokine (M/DC CR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New chemokines, TECK, MIP-3 alpha, MIP-3 beta, DC CR and M/DCCR, useful for treating conditions associated with abnormal physiology or development, including inflammatory conditions (e.g. asthma), and abnormal proliferation.
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The invention relates to a substantially pure or isolated polypeptide comprises the mature protein of human TECK (thywnus expressed chemokine) whose full length sequence appears as ADG67837. Also included are an isolated or recombinant nucleic acid encoding mature TECK, an expression vector comprising the nucleic acid, a host cell comprising the expression nector and a method for producing the polypeptide. Also disclosed are the mouse TECK cDNA and protein, human chemokines MIP-3alpha and MIP-3beta (and their encoding cDNAs), and the cDNAs and encoded proteins corresponding to human chemokine DCCR (dendritic cell receptor chemokine). The polypeptide is useful for treating conditions associated with abnormal physiology or development, including inflammatory receptors receptors MDCCR.
                                                                                                                                                                                                                                                        Human; 88; gene; thymus expressed chemokine; TECK; MIP-3alpha; MIP-3beta; chemokine receptor; DCCR; dendritic cell receptor for chemokine; M/DCCR; Monocyte/dendritic cell receptor for chemokine; abnormal physiology; development; inflammatory condition; asthma.
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                                                                                                                                                                                                       Human cDNA encoding chemokine receptor M/DCCR
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49. .1119
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96US-0028329P.
97US-0048593P.
97US-00887977.
                              ADQ67844 standard; cDNA; 1547
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GISH K C.
SCHALL T J
VICARI A.
ZLOTNIK A.
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04-JUN-1997;
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                                                                                          ADQ67844;
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Query Match
100.0%; Score 1035;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1035; Conservative 0; Mismatches

DB 12; Length 1547;

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ADQ38349 standard, DNA; 1646 BP.

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GCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGTTTCCATCTGCGTAGTAAC 1044
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The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual sequence of the sneed with an any one of the nucleic acids, where the presence of the SNP is correlated with an configuration in the individual. The invention further comprises an isolated nucleic acid molecule comprising at least correlation or its complement and encoding any one of the amino acid sequence given in the specification; an isolated polypeptide of that specification in the specification; an antibody comprising an amino acid sequence given in the specification; an antibody comprising an amino acid sequence given in the specification; an antibody comprising an amino acid sequence given in the specification; an amplified polymucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in concluding an amino acid sequence given in the specification and which is between about 16 and 1000 nucleotides in concluding an agent useful in treating or preventing an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and concluding an agent useful in treating or preventing or preventing or preventing or preventing an individual who has an increased or decreased risk for developing myocardial infarction. The sequence was not shown in the specification much of the invention or sequence was not shown in the specification. The sequence was not shown in the specification or the sequence has come from a electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                                                                                             Myocardial infarction, detection, single nucleotide polymorphism; SNP; cardiant; gene therapy; human; gene; ds.
                                                                                                                       Human SNP containing myocardial infarction-associated gene, SEQ
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30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
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                                                                                                                                                                                                                                                                                                                                                    22-DEC-2003; 2003WO-US040978
                                                                              (first entry)
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P-PSDB; ADQ39177.
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                                                                              18-NOV-2004
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ATGGCCAATTRCACGCTGGCACCAGAGGATGAATATGATGTCCTCATAGAAGGTGAACTG 261
                                        GIGCCAICACTCTGCTCTGCTGTTTGTGATCGGTGTCCTGGACAATCTCCTGGTTGTG
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The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's caltered risk for myocardial infarction in the individual. The invention further comprises an isolated nucleic acid molecule comprising at least schriber comprises an isolated nucleic acid molecule comprising at least schriber specification or its complement and encoding any one of the amino acid sequence given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody comprising an amino acid sequence given in the specification; an antibody comprising the polypeptide or its antigen-binding fragment; an amplified polymucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in comprising the collenging an agent useful in treating or preventing an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a nucleic acid molecule; a method of detecting a variant polypeptide; and myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The movel decreased risk for developing myocardial infarction and for preventing a composition for treating or preventing myocardial infarction. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          composition for treating or preventing myocardial infarction. This polymucleotide sequence represents a human myocardial infarction-seasociated gene containing one or more SNPs of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.
                                                                                                                                                                            Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human; gene; ds.
                                                                                                                               Human SNP containing myocardial infarction-associated gene, SEQ ID 13
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ADQ38350 standard; DNA; 1776 BP
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10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
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New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for Human, probe, 88, gene expression, single exon probe, microarray, alternative splicing event, genomic alteration. Human genome derived single exon probe #22780. Claim 1; SEQ ID NO 22780; 80pp; English. ACH89585 standard; DNA; 1140 BP 었 03-APR-2002; 2002US-00029386 03-APR-2002; 2002US-00029386 Hanzel (first entry) (PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K. WPI; 2004-119264/12 Penn SG, Rank DR, surveying tissues. US2003194704-A1. Homo sapiens, 29-JUL-2004 16-OCT-2003 ACH89585

The invention relates to a nucleic acid probe for measuring human gene sequences in the specification, or their complements or fragments, and sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acids sequences (c) claim at least 8 amino acids of any of the 6888 amino acids sequences (c) in the specification. The probe is a single acon probe that chybridises under high stringency conditions to a nucleic acid molecule expression (comprising a plurality of single exon nucleic acid probes for measuring human calls or tissues. Also included are a spatially.

CC daressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon addressably isolatable or amplifiable from the plurality), a single con microarray for measuring human gene expression, a wector comprising the single exon probe cited above, where each of the plurality of probes is single exon microarray for measuring human gene expression, a vector comprising the single exon probes cited above, an ORP-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid solated antibody that binds specifically to a peptide cited above, methods of salling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable correspondent including data on the expression of a single exon microarrays.

CC ited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may apparatus are useful in gene expression analysis. The probes may apparatus are useful in gene expression analysis. The probes are useful and characterising gross alterative splicing events, in detecting and characterising gross alterative splicing events, in detecting and characterising gross alterations in the probes are useful the sequence data for this adjunct of the probes of segdata.uspto.gov/sequence.html?DocID=20030194704

Sequence 1140 BP; 294 A; 275 C; 241 G; 330 T; 0 U; 0 Other;

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RESULT 7 ACH89585

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Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J,
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
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17-AUG-2000;
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07-SEP-2000;
18-SEP-2000;
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 Score 1031.8;
Pred. No. 0;
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99.74;
                 Best Local Similarity 99.8
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Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnezary; antiartexiosclerotic; PRO agnorist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
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2001US-00808689.
2001US-00816744.
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989 ACCCCACTTCAACCCAGGGGGGAGTCTGCACAAGGCACATCGAGGAAGAACCTGACCAT 1048
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      TCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTGGACAAA
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                                                   GTGCAAATGAGAAAAACACTAAGGTTCAGGGAGCAGAGGTATAGCCTTTTCAAGCTTGTT
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24-OCT-2000;
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22-JAN-2001;
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02-AUG-2000;
17-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCCCAGGCACTCTCAGCCCAGCTG 120
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                                                                                        One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mapping. ABL88259 to ABL88267 represent F
exemplification of the present invention
                                                                                                                                                                                Claim 2; Fig 15; 565pp; English
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Matches 1033; Conservative
                                                                                        One hundred and eighty
                         2002-090516/12
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Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
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99.7%; Score 1031.8; DB 6; Length 1475;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1033; Conservative 0; Mismatches 2; Indels 0;
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28-FEB-2001; 2001US-00796498.
28-FEB-2001; 2001WO-US006520.
01-MAR-2001; 2001WO-US006666.
09-MAR-2001; 2001US-00802706.
14-MAR-2001; 2001US-00802706.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854208.
10-MAY-2001; 2001US-00866228.
25-MAY-2001; 2001US-00866034.
25-MAY-2001; 2001WO-US017092.
30-MAY-2001; 2001WO-US017092.
30-MAY-2001; 2001WO-US017092.
30-MAY-2001; 2001WO-US017092.
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GERRITSEN M E.
GODDARD A.
GODOWSKI P J.
GURNEY A L.
HILLAN K J.
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BAKER K P.
FERRARA N.
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PAONI N F.
STEPHAN J F.
WATANABE C K.
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cardiovascular disorder; endothelial disorder; anglogenic disorder; myocardial infarction; cardiac hypertrophy; trauma; cancer; age-related macular degeneration; anglogenesis; endothelial cell apoptoclas; smooth muscle cell growth; endothelial cell tube formation.
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J, Hillan KJ, Marsters SA, Pan J,
PM, Wood WI, Ye W;
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20-JUN-2001; 2001WO-US01735.
09-JUL-2001; 2001WO-US021735.
20-FEB-2002; 2002US-00081056.
                                                                                                                                                               16-AUG-2002; 2002US-00223084
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Godowski PJ, Gurney AL, Hi
Watanabe CK, Williams PM,
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P-PSDB; ADD10305.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The inventioh relates to an isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded cacid, or an agonist or antagonist, is used to treat a cardiovascular, endothelial, or angiogenic disorder in a mammal, protectably a human. The human may have suffered a myocardial infarction or has cardiac hypertrophy, trauma, a cancer, or age-related macular degeneration. The cardiac hypertrophy is characterised by the presence of an elevated level of PGF-2 alpha. A PRO polypeptide, given in the specification, or an agonist is used to inhibit or stimulate endothelial cell growth in a mammal. PRO21 or an agonist is used to induce cardiac hypertrophy. PRO1376 or PRO1499 is used to stimulate angiogenesis. PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO polypeptide, given in the specification, or an agonist is used to induce endothelial cell upoptosis. A PRO polypeptide or inhibit smooth muscle cell growth, or to induce endothelial cell tube formation. The present sequence represents a cDNA encoding a CMC or an agonist is a cDNA encoding a CMC or an agonist cell tube formation.
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Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid encoding a secreted and transmembrane polypeptide, useful for treating a cardiovascular, endothelial, or angiogenic disorder in a mammal, such as cancer or age-related macular
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0; Mismatches
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09-JUL-2001; 2001WO-US021735.
20-FEB-2002; 2002US-00081056.
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  AATTGCCTTCTGACTGTGCAAAGGTACCTAGTGTTTTTGCACAAGGGCAACTTTTTCTCA
                                                         GCCAGGAGGAGGCCCTGTGGCATCATTACAAGTGTCCTGGCATGGGTAACAGCCATT
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5, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PM, Wood WI, Ye W;
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; SEQ ID NO 15; 492pp; English.
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20-JUN-2001; 2001WO-US019692.
09-JUL-2001; 2001WO-US021735.
20-PEB-2002; 2002US-00081056.
                                        16-AUG-2002; 2002US-0022308B.
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Watanabe CK, Williams PM,
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Best Local Similarity 99.8
Matches 1033; Conservative
                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                           Ferrara N,
                                                                                                                                                                                                                                                                                                          WPI; 2003-829354/77.
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05-JUN-2003
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569 IGIGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTCTGGAAGCATTTTCTG
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                                                                                                                                                                         ACTITAAAAATGAACATTTCGGTTCTTGTCCTCCCCCTTTTATTTTACATTTCTTAT
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Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; PRO; gene; se; cardiovascular disorder; endothelial disorder; anglogenic disorder; endothelial cell growth; cardiac hypertrophy; cell apoptosis; cell tube formation; anglogenesis; smooth muscle cell growth; myocardial infarction; trauma; cancer; agge-related macular degeneration; cytostatic; cardiant; cerebroprotective; ophthalmological; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH43448 standard; cDNA; 1475
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                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid encoding a secreted and transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded by the nucleic acid, or an agonist or antagonist, is used to treat a cardiovascular, endothelial, or anaglogenic disorder in a mammal, preferably a human. The human may have suffered a myocardial infarction or has cardiac hypertrophy, trauma, a cancer, or age-related macular or specification. The cardiac hypertrophy is characterised by the presence of an elevated level of PGF-2 alpha. A PRO polypeptide, given in the specification, or an agonist is used to inhibit or stimulate endothelial cell growth in a mammal. PRO21 or an agonist is used to induce cardiac hypertrophy. PRO1376 or PRO1499 is used to stimulate angiogenesis. PRO4102 or an agonist is used to induce endothelial collypeptide, given in the specification, or an agonist is used to induce endothelial cell apoptosis. A PRO polypeptide, given in the specification, or an agonist is used to induce endothelial cell aboptosis. A PRO cell tube formation. The present sequence represents a cDNA encoding a
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                                                                                                                 Stephan JF;
                                                                                                                                                                                                                                     New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO205 or PRO214, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and for treating disorders involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCCAGGCACTCTCAGCCCAGCTG
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                                                                                               Gerber H, Gerritsen ME, Goddard A;
,, Hillan KJ, Marsters SA, Pan J,
PM, Wood WI, Ye W;
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                                                                                                                                                                                                                                                                                                                                      Claim 2; SEQ ID NO 15; 492pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.7%;
09-JUL-2001; 2001WO-US021735.
20-FEB-2002; 2002US-00081056.
                                                                                                                 Godowski PJ, Gurney AL, H
Watanabe CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 1033; Conservative
                                                         (GETH ) GENENTECH INC
                                                                                                   Ferrara N,
                                                                                                                                                                             WPI; 2004-008957/01.
P-PSDB; ADE41266.
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ACCCCACTTCAACCCAGGGGCAGTCTGCACAAGGCACATCGAGGGAAGAACCTGACCAT 1020
                                       TCCACTITICAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGTTTCTTGATGGGACATTTAGCAATACCTCTGCCGCTGTTTCCATCTGCGTAGTAAC
                                                                                                                                                                                                 TTIGCCATAATGGTAGTCTTCCTTCTGATGTGGGCGCCCTACAATATTGCATTTTTCCTG
                                                                                                                                                                                                                                                       TCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGCAGCTACAATCTGGACAAA
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                                                                                                 GTGCAAATGAGAAAAACACTAAGGTTCAGGGAGCAGAGGTATAGCCTTTTCAAGCTTGTT
                                                                                                                                     GTGCAAATGAGAAAAACACTAAAGGTTCAGGGAGCAGAGGTATAGCCTTTTCAAGCTTGTT
                                                                                                                                                                         TITGCCGTAATGGTAGTCTTCCTTCTGATGTGGGCGCCCTACAATATTGCATTTTTCCTG
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98US-00180997.
98WS-US025108.
99WS-00218517.
99WS-00214186.
99WS-0025411.
99WS-00254460.
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98US-00015089.
98WO-US018824.
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98WO-US019330
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22-DEC-1998;
05-JAN-1999;
12-PEB-1999;
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19-NOV-1998
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                                                                                                                                                                                                   The invention relates to human PRO polypeptides and the PRO polynucleotides encoding them. The invention also relates to treating cardiovascular, endothelial or angiogenic disorders in mammals, inhibiting endothelial cell growth, stimulating endothelial cell growth, stimulating endothelial cell growth, inhibiting cardiac hypertrophy, cell apoptosis or cell tube formation and stimulating angiogenesis or smooth muscle cell growth by administering polypeptides of the invention. The PRO polypeptides and polynucleotides are useful for treating cardiovascular, endothelial or angiogenic disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma, cancer or age-related macular degeneration. The PRO polynucleotides are useful as hybridisation probes in chromosome and gene mapping and in generating antisense RNA and DNA, and for chromosome identification and tissue typing. The PRO polypeptides and polynucleotides are also useful in gene therapy and as melecular weight markers for protein electrophoreals purposes. This sequence represents a human PRO polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGAGCGATGAGGCAGAGCAATGTGACAAGTATGACGCCCAGGCACTCTCAGCCCCAGGTG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGTITCTAACTIGTGTTTCTTGCTTACCTGCCCTTCTGGGCTCATGCTGGGGGCGAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGCCATCACTCTGCTCTGTGTTTGTGATCGGTGTCCTGGACAATCTCCTGGTTGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGCCATCACTCTGCTCTGTGTTTGTGATCGGTGTCCTGGACAATCTCCTGGTTGTG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATTIGCCTTCTGACTGTGGAAAGGTACCTAGTGTTTTTGCACAAGGGCAACTTTTTCTCA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCAGGAGGAGGGTGCCCTGTGGCATCATTACAAGTGTCCTGGCATGGGTAACAGCCATT 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTACAGTGAGACATTTTTC 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATTGCCTTCTGACTGTGCAAAGGTACCTAGTGTTTTTGCACAAGGGGAACTTTTTCTCA 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGCCACTTTGCCTGAATACGTGGTTTATAAACCTCAGATGGAAGACCAGAAATACAAG 568
                                                                                           polypeptides and nucleic acids encoding the polypeptides, useful sting myocardial infarction, cardiac hypertrophy, trauma, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGCCCAATTACACGCTGGCACCAGAGGATGAATATGATGTCCTCATAGAAGGTGAACTG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGCCCAATTACACGCTGCCACCAGAGGATGAATATGATGTCCTCATAGAAGGTGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCATGTGTAAAATTCTCATTGGACTGTACTTCGTGGGCCTGTACAGTGAGACATTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTCTGGAAGCATTTTCTG
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 Ye W;
Watanabe CK, Williams PM, Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1031.8;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                       Claim 2; SEQ ID NO 15; 492pp; English
                                                                                                                                   or age-related macular degeneration.
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Matches 1033, Conservative
                                       WPI; 2004-042166/04.
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Stephan JF,
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06-JAN-2000;
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05-APR-2001;
25-MAY-2001;
25-MAY-2001;
      12-APR-1999
02-JUN-1999
14-JUN-1999
14-JUN-1999
25-AUG-1999
08-SEP-1999
11-SEP-1999
15-SEP-1999
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15-SEP-1999
16-OCT-1999
16-OCT-1999
18-OCT-1999
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16-DEC-1999;
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30-DEC-1999;
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09-MAR-2001;
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The invention relates to human PRO polypeptides and the PRO polymucleotides encoding them. The invention also relates to treating polymucleotides encoding them. The invention also relates to treating cardiovascular, endothelial or angiogenic disorders in mammals, inhibiting endothelial cell growth, stimulating endothelial cell growth, stimulating endothelial cell growth by administering inducing cardiac hypertrophy, cell apoptosis or cell tube formation and polympeptides of the invention. The PRO polypeptides and polymucleotides are useful for treating cardiovascular, endothelial or angiogenic are useful for treating cardiovascular, endothelial or angiogenic clascular despensation, The PRO polymucleotides are useful as hybridisation probes in chromosome and gene mapping and in useful as hybridisation probes in chromosome and gene mapping and in generating antisense RNA and DNA, and for chromosome identification and tissue typing. The PRO polypeptides and for chromosome identification and tissue typing. The PRO polypeptides and for chromosome are also useful in gene therapy and as molecular weight markers for protein and electrophoresis purposes. This sequence represents a human PRO polymucleotide of the invention. Note: The sequence data for this patent is also available in electropic format from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                       KJ, Marsters SA, Pan J, Stephan JF; WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 ATGCCCAATTACACGCTGGCACCAGGATGAATATGATGTCCTCATAGAAGGTGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGGCCAATTACACGCTGGCACCAGAGGATGAATATGATGTCCTCATAGAAGGTGAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 PRO21383, useful in molecular biology, chromosome and gene mapping, generating antisense RNA and DNA, and in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1031.8; DB 12; Length 1475;
Pred. No. 0;
0; Mismatches 2; Indels 0; (
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                                                                                                                                                                                                                                                                                                                                                                                                         Gerritsen ME,
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AL, Hillan K
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                                                                     13-MG-2001; 2001US-00929404.
16-MG-2001; 2001US-00931836.
28-MG-2001; 2001US-00941992.
04-SEP-2001; 2001US-00946374.
07-SEP-2001; 2001US-00946871.
15-NOV-2001; 2001US-00001054.
06-DEC-2001; 2001US-00006867.
19-DEC-2001; 2001US-00006867.
15-JAN-2002; 2001US-00052866.
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2001US-00927796.
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Best Local Similarity 99.8%;
Matches 1033; Conservative
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Godowski PJ, Gurney AL, F
Watanabe CK, Williams·PM,
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P-PSDB; ADK82794.
09-JUL-2001;
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301 CCCATGGGTAAAATTCTCATTGGACTGTACTTGGGGCCTGTACAGGGGAACATTTTCC 369 319 AATTGCCTTCTGACTGTGCAAAGGTACCTGTGTTTTTGCAAAGGGGAACATTTTTCC 329 311 AATTGCCTTCTGACTGTGCAAAGGTACCTGTGTTTTTGCAAGGGGAACATTTTTCC 329 312 CCCATGGTAAAATTCTCATTGGACTGTTTTTGCAAGGGCAACTTTTTTCC 420 313 AATTGCCTTCTGACTGTGCAAAGGTACCTGTGTTTTTGCAAGGGCAACTTTTTTTCC 420 314 AATTGCCTTCTGACTGTGCAAAGGTACCTGTGTTTTTGCAAGGGCAACTTTTTTTCC 420 315 AATTGCCTTCTGACTGTGCAAATTGCTGATTAAAACTCTGGAAGGTAAAAAGG 540 316 CCCAGGAGGAGGGGCCCTGTGGGCATTAAAACTCTGGAAGGTAAAAAGG 540 317 GCCAGAAGGAGGAGCCTTTCTGCTGTTTTTTAAAAATTGAAATTTTTAAAAATTGCAAATTTTTTTT	a			28
313 CCATACHTAGATTCTATTGATCTATTGATCGACCTATACATTGATCGACCTATACATTGATCGACCTATTTCCA 420 319 AATTGCCTTCTGACTGCAAAGGTACCTAGTGTTTTTGACGCAACGTTTTTCCA 420 319 AATTGCCTTCTGACTGTGCAAAGGTACCTAGTGTTTTTTGACGCAACGCCAACTTTTTCCA 420 421 GCCAGGAGGAGGGTCCCCTGCCACCTATTACAACTCTCACACAAAAAACAACAATTGACAAAAAACAAAAAACAAAAAAAA	8			09
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421 GCCAGAGGGGGCCCCTGTGCCATTACAAGTGCTCCTGGCATGGCTAAT 480 419 GCCAGAGGGGGCCCTGTGCCATTACAAGTGCTCTGGCATGGGTAACAGCCATT 508 410 GCCAGAGGGGGCCCTGTGCGATTACAAGTGCTCTGGCATGGGTAACAGCCATT 508 411 GCCAGGAGGGGCCCTGTGCGGTTTATACAAGTGCTCTGGGAACAACAGCCATT 508 541 TGTGCCATTTACAAAAACCCTTCCTGCCAGCTGATGAGACATTTCTG 609 552 TGTGCATTTACAAAACCCTTCCTGCCAGCTGATGAGAATTTCTG 628 653 TGTGCAATTTACAAAACCCTTCCTTCCTGCCAGCTGATGAGCATTTTTCTTTACATTTTCTTTTACATTTCTCTTAT 609 654 TGTGCAATTTACAAAAACCTTACGGTTCTTGTCCTCCCCCTATTTATT	දි සි			20 4 8
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481 CTGGCCACTTTGCCTGAATTCGTGGTTTATAAACCTCGGAATGGAAGACCAGAAATACAG 568 509 CTGGCCACTTTGCCTGAATACGTGGTTTATAAACCTCGGAATGGAAGACCAGAAATACAG 568 541 TGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTTTTTTCTG 609 569 TGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTTTTTTT	. A			80
509 CTGGCCACTTTGCCTGATACCTCGCCGCTGATGGAAGCCACTTGCGGAAATACCGG 600 541 TGTGCATTTAGCAGAACTCCCTTCCTGCCAGCTGATGAGACATTTTTGGAAGCATTTTTG 600 1	È			40
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689 GYGCAAATGAGAAACACTTCTGAGGTCGAGGGGGGGCTTTTTCAGGCTTTTTCCTG 780 721 TTTGCCGTAATGGTGCTCTTCTGATGTGGGGGCCCTACAATATTGCATTTTTCCTG 780 781 TCCACTTTCAAGGAGCTCTTCTGATGTGGGGGCCCTACAATATTGCATTTTTCCTG 808 781 TCCACTTTCAAAGACACTTCTCCTTGATGTGGGCGCCCTACAATATTGCATTTTTTCCTG 808 781 TCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCAAGAGAGCAGCTACAATTTTTCCTG 808 781 TCCACTTTCAAAGAACACTTCTCCCTGAGTGACTGCCAAGAGAGCAGCTACAATTTTTCCTG 808 841 AGTGTTCAAACACACAAACTCCTCCCCACTGCTGCTACAACCTCTCTGAACAAA 868 841 AGTGTTCAACACAAAACTCATCGCCACCACCACTGCTGCAACAACCTCTCTTTTTTTT	È			20
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capable of being expressed on brain glial cells and is known in the mouse as L-CCR or in humans as CRAM-B. The chemokine receptor expressed in a cultured cell comprising the cell transfected with a nucleic acid and a HER cell, is useful in identifying a candidate drug compound for treating inflammatory or degenerative brain disease, e.g. ischaemia, Alzhaimer's firstaamse or multiple sclerosis. The agonist or antagonist is useful in the preparation of the pharmaceutical composition useful in treating neurodegenerative and neuroinflammatory diseases such as allergic encephalitis and chronic obstructive pulmonary disease and obstructive airway diseases such as asthma. This sequence represents human CRAM-B cDNA, also known as CCR12
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                            901 GCGTTTCTTGATGGGACATTTAGCAAATACCTCTGCCGCTGTTTCCATCTGCGTAGTAAC
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inflammatory conditions including asthma.
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The invention relates to nucleic acids encoding the chemokines TECK, MIP-Jalpha, MIP-Jbeta, DC CR and M/DC CR. The polypeptide sequences are useful in isolating DNA clones encoding the chemokines, for generating antibodies, and for predicting oligonucleotides for screening a library to isolate species variants. A nucleic acid encoding a chemokine polypeptide can be used to identify genes, mRNA and cDNA species which encode related or homologous ligands, as well as DNA encoding homologous proteins from different species. The chemokines and antibodies which to the polypeptides are useful in the treatment of conditions associated with abnormal physiology or development, including inflammatory degeneration and atrophy. This sequence represents cDNA encoding the human monocyte/dendritic cell receptor for chemokine (M/DC CR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene, 88; thymus expressed chemokine; TECK; chemokine; MIP-3alpha; MIP-3beta; dendritic cell receptor for chemokine; DC CR; M/DC CR; asthma; monocyte/dendritic cell receptor for chemokine; inflammatory condition; abnormal proliferation; degeneration; atrophy; antinflammatory, antiasthmatic; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Human monocyte/dendritic cell receptor for chemokine (M/DC CR) cDNA
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